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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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greater than or equal to the score of the result being printed, 
s derived by analysis of the total score distribution.
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               Issued_Patents_NA: *
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Copyright (c) 1993 - 2002 Compugen Ltd
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US-08-323-430-9
US-08-471-570-15
US-07-947-680-15
US-08-401-323-18
US-08-401-323-18
US-08-401-323-18
US-08-401-323-18
US-08-521-623-10
US-08-521-623-10
US-08-321-430-10
US-08-321-430-10
US-08-321-430-11
PGT-089-60-331-4
US-08-321-430-11
           PCT-US93-03256-6
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(without alignments)
13088.964 Million cell updates/sec
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TION: ITON: NUME: 144 ITON: 147 ITON: 147 ITON: 147 ITON: NUME: 147 ITON: NUME	NDENCE ADDRESS SEE: Rhone-Fo SEE: SOO Arcola Collegeville PA 19426 19426 ING STEE: Ploppy ER: IBH PC co. ING STEE: Patentn: PA RE: Patentn DA APPLICATION DA APPLICATION DA	ILT 1  18-451-822A-9/c  10-16-16-18-19-18-19-18-19-18-19-18-19-18-19-18-19-18-19-18-19-18-19-18-19-18-19-18-18-18-18-18-18-18-18-18-18-18-18-18-	000000000000000000000000000000000000000
-MAY-1995 435-MAY-1995 435-MAY-1995 435-MAY-1996 DATA: US 08/3 DATA: US 08/3 DATA: US 07/5 -NGC-1992 DATA: US 07/5 -NGC-1992 MAT-LIN -WANT-LIN -WUNDER: 29,699 -MAT-LIN -WUNDER: 29,699 -MAT-LIN -WUNDER: 29,699 -MAT-LIN -	RESS:  REPOULENC Re-Poulenc Re-Po	Personal Contraction of the Cont	40444004444000000000000000000000000000
123,4 49,5	Rorer Legal Department  the symbols see #1.0, Version #1.25	ALIGNMENTS	PCT-US93-03256-11 US-09-520-542-19 US-09-306-290-3 US-08-686-9908-9 US-09-306-290-3 US-08-686-9908-9 US-09-146-334-13 US-08-687-9904-16 US-08-757-024-16 US-08-757-024-13 US-08-757-024-19 US-08-757-024-19 US-08-757-024-19
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                                                 US-08-471-570-15/c
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US-08-323-430-9
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                 Sequence 15, Application US/08471570 Patent No. 5750371
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Best Local Similarity
Matches 33; Conserv
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Patent No. 6344546
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Crumley, Greg
APPLICANT: Jaye, Michael C
APPLICANT: Schlessinger, Joseph
                                                                                                                                         2707 TATCCACACATAAACGGCAGTGTTAAAACATGA 2739
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-7UL-1990
ATTORNEY/ACENT_INFERNATION:
AUTORNEY/ACENT_INFERNATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-EDS/MS-DOS
CURRENT APPLICATION DATA:
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ADDRESSEE: Rhone-Poulenc Rorer Legal Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Fibroblast Growth Factor Receptors NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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CITY: Collegeville
STATE: PA
                                                                                                                        33 TATCCACACATAAACGGCAGTGTTAAAACATGA 1
                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
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Similarity 100.0%; Pred. No. 26;
33; Conservative 0; Mismatches
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Best Local Similarity 84.6%;
Matches 33; Conservative
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TELECOMMUNICATION INFORMATION:
TELECHIONE: (617)523-3400
TELECAX: (617)523-6440
TELECAX: (2029) STRE UR
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                    GENERAL INFORMATION
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APPLICATION NUMBER: US 07/743369
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LIMEK, Ernest V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
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                                                                                                                                                             NUMBER OF SEQUENCES: 1
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                                                                                        CITY: HOUSTON
STATE: TEXAS
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    COMPUTER:
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    IBM PC COMPATIBLE
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: MOLECULE TYPE: other nucleic acid, synthetic DNA US-08-471-570-15
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APPLICANT: WILSON, STEVEN E.
TITLE OF INVENTION: METHODS AND TREATMENTS FOR
TITLE OF INVENTION: AND KERATINOCYTE GROWTH FACTORS
TITLE OF INVENTION: AND KERATINOCYTE GROWTH FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
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                                                                                                                                                                                                                                                                                                                     39 GARATGGARATGATGAARATGATCGGGAAGCATAAGAAT 1
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Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.7%; Score 30; DB Best Local Similarity 100.0%; Pred. No. 1. Matches 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Wilson, Steven E.
TITLE OF INVENTION: Methods:
TITLE OF INVENTION: Healing:
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: NOT APPLICABLE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                   NFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 0750:311/KIT
TELECONMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEPAX: 512-474-7577
TELEX: NOW PAGE 1757
                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0:
FILING DATE: 09-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1242 GATTGAGGTTCTCTATATTCGGAATGTAAC 1271
                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                    TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL, BARBARA S.
REGISTRATION NUMBER: 33,92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                      TELEFAX: (512) 474-7577
TELEX: 79-0924
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 GATTGAGGTTCTCTATATTCGGAATGTAAC 1
                                 STRANDEDNESS:
                                                                 LENGTH:
                                                                                                                                                                                      NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P. O. CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
FILING DATE: SEPTEN
CLASSIFICATION: 514
              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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SOFTWARE: WORDPER
                                                nucleic acid
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                                                               30 base pairs
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linear
                linear
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                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Healing with Growth Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
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Query Match

0.78;

Score 30;

BG

1;

Length 30;

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RESULT 7
US-07-997-133-4/c
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APPLICATION NUMBER: US/07/642,755
FILLING DATE: 18-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 528855man F.
REGISTRATION NUMBER: 24,618
REFERENCE/OCKET NUMBER: 7769-226-0
TELECOMMUNICATION INFORMATION:
TELEX: 248855 OPAT UR
INFORMATION FOR SED ID NO. 4:
SEQUENCE CHARACTERISTICS:
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US-07-997-133-4/c
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                                                  Sequence 4, Application US/07997133 GENERAL INFORMATION:
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Best Local Similarity
Matches 27; Conserv
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Matches 30; Conservative (
              APPLICANT:
                                                                                                                                                                                     2488 TGTTGGCATGCAGTGCCCTCCCAGAGACC 2516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION NUMBER: US/07/997.1:
FILING DATE: 28-DEC-1992
                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sarmientos, Paolo
TITLE OF INVENTION: Extracellular Form of the Human
TITLE OF INVENTION: Fibroblast Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bergonz
APPLICANT: Mazue,
APPLICANT: Isacchi
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                   30 TGCTGGCATGCAGTGCCCTCACAGAGACC 2
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia ZIP: 22202
                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION
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                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                30 base pairs
Isacchi, Antonella
                Mazue, Guy
                               Bergonzoni, Laura
                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bergonzoni, Laura
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                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                          0.6%;
93.1%;
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Pred. No. 1.5e+03;
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0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 4
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%;
Best Local Similarity 93.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703)486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                            APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibilashvilli, Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2488 TGTTGGCATGCAGTGCCCTCCCAGAGACC 2516
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LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, Norman F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/642,755
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Sarmientos, Paolo
APPLICANT: Sarmientos, Paolo
TITLE OF INVENTION: Extracellular Form of the Human
TITLE OF INVENTION: Fibroblast Growth Factor Receptor
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
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ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
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STRANDEDNESS:
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REGISTRATION NUMBER:
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  SOFTWARE:
                  OPERATING SYSTEM:
                                                                                                               COUNTRY:
                                                                                                                                       STATE:
                                                                                                                                                       CITY: Menlo Park
                                                                                                                                                                          ADDRESSEE: Fish & Richardson, P.C. STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                        431, Application US/08859998
o. 5994076
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FastSEQ for Windows Version 2.0
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Pred. No. 1
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US-08-859-998-432/c
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Best Local Similarity 100.0%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 432, Application US/08859998 Patent No. 5994076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvilli, Re
APPLICANT: Bibilashvilli, Re
TITLE OF INVENTION: METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-884-0875
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                 TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                APPLICATION NUMBER: US FILING DATE: 21 MAY-19 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                     REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA
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PRIOR APPLICATION DATA:
                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Field, Bret E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                        NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson, P.C. STREET: 2200 Sand Hill Road, Suite 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GCTCCATGCTGTGCCTGCGGCCAAC 25
                                                                                                                                                                                                                                                                                                                                                                                         94025
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VENTION: METHOD OF ASSAYING DIFFERENTIAL
                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bret E.
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100.0%; Pred. No. 2.1e+(
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                                                                                           09096/002001
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                                                                       Query Match
Best Local :
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GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 431:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1179 GCCCGACGGGCTGCCCTACCTCAAG 1203
               768 GCTCCATGCTGTGCCTGCGGCCAAC 792
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                                                     Local Similarity
hes 25; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM KINDOWS5
OPERATING SYSTEM KINDOWS5
CURRENT APPLICATION DATE
PLILING DATE: 05-Jan-1999
CLASSIEICCTION: CANKNOWN
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION UNBER: 08/859,998
APPLICATION WIBER: 08/859,998
FILING DATE: 21 - MAY - 1997
ATTORREY_AGENT_INFORMATION:
NAME: FIRST INFORMATION: 07/620
REFERENCE_DOCKET_NUBER: 07/620
REFERENCE_DOCKET_NUBER: 09/96/002001
                                                                                                                                       OTHER INFORMATION: oligonucleotide primer SEQUENCE DESCRIPTION: SEQ ID NO: 431:
                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                 MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 415-322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish, & Richardson, P.C.

STREET: 2200 Sand Hill Road, Suite 100

CITY: Menio Park

STATE: CA
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Jokhadze, George
Bibilashvilli, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bibilashvilli, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-854-0875
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                                                  Conservative
                                                                    100.0%;
                                                               0.6%; Score 25; DB 4;
100.0%; Pred. No. 2.1e+03
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100.0%; Pred. No. 2.1e+(
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                                                  0; Indels
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OTHER INFORMATION: oligonucleot
; SEQUENCE DESCRIPTION: SEQ ID NO: 432:
US-09-225-928-432
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US-08-451-822A-10
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                                                                                                                                                        Sequence 10, Application US/08451822A Patent No. 5863888
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Matches 25; Conserv
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GENERAL INFORMATION:
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                GENERAL INFORMATION:
APPLICANT: Dionno, Craig A
APPLICANT: Dionno, Craig A
APPLICANT: Crunley, Gree
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 432:
                                                                                                                                                                                                                                                                                                                 1179 GCCCGACGGGCTGCCCTACCTCAAG 1203
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             25 GCCCGACGGGCTGCCCTACCTCAAG 1
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LENGTH: 25 base pairs
TYPE: nucleic acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMHUNICATION INFORMATION:
TELEPHONE: 415-22-3070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/859,998 FILING DATE: 21-MAY-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Lin
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bibilashvilli, Robert TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chenchik, Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Menlo Park
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson, P.C. STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                             Conservative
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Bibilashvilli, R
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
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RESULT 13
US-08-323-430-10
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                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6344546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/5
FILING DATE: 21-NG-1992
PRIOR APPLICATION DATA: 37/5
APPLICATION NUMBER: US 07/5
FILING DATE: 06-7UL-1990
ATMORREY/ACENT IMPORMATION: NAME: SEVICEKY, MARLIA
REGISTRATION NUMBER: 29.69)
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                            NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Legal Department
                                                                                                                                                                                                                                                                    APPLICANT: Dionne, Craig A
APPLICANT: Cramley, Greg
APPLICANT: Jave Michael C
APPLICANT: Jave Michael C
APPLICANT: Schiessinger, Joseph
TILE OF INVENTION: Fibroblast Growth Factor Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: A0496E
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 14-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/323,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 ACCATGGTCAGCTGGGGTCGTTTCA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 26-MAY-1995
                                                                                                                                 COUNTRY:
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                                                                                                                                                         STATE:
                                                                                                                                                                      CITY: Collegeville
                                                                                                                                                                                              STREET:
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                                                                                                                                                                                            500 Arcola Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (610) 454-3808
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                                                                                                                                      USA
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US-08-371-001-4
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US-08-371-001-4
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Patent No. 5783683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 25; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US to be assign
FILING DARIE: 21-ANG-1992
APPLICATION NUMBER: US 07/549,587
FILING DARIE: 06-2011990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (215) 454-3808 INFORMATION FOR SEQ ID NO:
                                                                                                                                     TELEFAX: (619) 236-10
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                    COMPUTER REDABALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Morrison Ph.D., Richard TITLE OF INVENTION: Methods and ConTITLE OF INVENTION: Tumor Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: GOOdman, Rosanne
REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: A00
TELECOMMUNICATION INFORMATION:
                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 699-3630
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Brotman, Harris F.
REGISTRATION NUMBER: 35,4
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
MOLECULE TYPE: cDNA
                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 ACCATGGTCAGCTGGGGTCGTTTCA 295
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/371,001 FILING DATE: January 10, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 401 "B"
CITY: San Diego
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                                      TOPOLOGY:
                                                      STRANDEDNESS:
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                                                                         nucleic acid
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                                                                                                                                                        (619) 236-1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (215) 454-3817
                   Other Nucleic Acid
                                                      single
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Pred. No. 2.7e+0
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Search completed: December 11, 2002, 17:47:48 Job time: 105 secs
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US-08-451-822A-11/c
US-08-451-822A-11/c
Sequence 11, Application US/08451822A
Patent No. 5863888
Patent No. 5863888
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MEDIUM READABLE FORM:

MEDIUM REPORT STAR PROPPY disk

COMPUTER: STAR PROPPY disk

COMPUTER: STAR PROPPY disk

COMPUTER: STAR PROPPS AND STAR PROPERTY OF STAR PROPERTY ON MUNICIPATION WINDER:

PRICE APPLICATION WINDER: US 08/323,430

PRICE APPLICATION WINDER: US 08/323,430

PRICE APPLICATION WINDER: US 07/934,372

PRICE APPLICATION WINDER: US 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 24; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE, DOCKET NUMBER: A0496E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
                                                                                                                                            APPLICANT: Dionne, Craig A
APPLICANT: Crumley, Greg
APPLICANT: Crumley, Greg
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Pibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 AAGTGTGCAGATGGGATTAACGTC 230
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ZIP: 19426
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Maximum Match
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Perfect score:
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Maximum DB seq length: 50
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1. /SIDSJ/9cpdata/geneseq/geneseqn-embl/NA1981.DAT:*
2. /SIDSJ/9cpdata/geneseq/geneseqn-embl/NA1982.DAT:*
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17443:791 Million cell updates/sec
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	22	21	24	22	19	24	23	22	15	22							22	22	22	23	24	22	22	22	24	21	22	22	17	13	21	20	16	21	22	22
ALIGNMENTS	AAL29199	AAZ69037	AAS95731	AAL31043	AAV44045	ABN89414	AAS58336	AAF60897	AAQ66922	AAF98419	AAV41447	AAN71061	AAX52599	AAL28459 .	AAL31923	AAX84629	AAL30581	AAL30410	AAI30469	AAH88384	AAS95735	AAH20352	AAI75629	AAL28400	ABN75039	AAA64611	AAF58623	AAL28218	AAT31054	AAQ23620	AAZ66994	AAX52549	79	$\sim$	304	AAL29254
		3 7	TD.	SNP	Mouse bFGF recepto	Polymorphism detec	CDNA #1012 encodin	ate forming	Poly-dA 50mer prob	an cDNA	cleotide	robe for ex	Human genome biall	Human SNP oligonuc	Human SNP oligonuc	Oligomer used in D	Human SNP oligonuc	Human SNP oligonuc	Human single nucle	CNS disorder-relat	Allele discriminat	HHV6 virus p41 gen	Human silent SNP c	Human SNP oligonuc	Human aCl wt cMNR	AU rich sequence i	Murine C-kit exon				map-related	3	_	Human MSH6 fragmen	_	Human SNP oligonuc

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## ALIGNMENTS

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New fibroblast growth factor receptor proteins - treating gf-mediated conditions e.g. angiogenesis	WPI: 1992-056827/07. P-PSDB: AAR20750.	Dionne CA, Crumley G, Jaye MC, Schlessinger J;	(RORE ) RORER INT HOLDINGS.	06-JUL-1990; 90US-0549587.	03-JUL-1991; 91WO-US04745.	23-JAN-1992.	W09200999-A.	יייייייייייייייייייייייייייייייייייייי	000 + 100 + 100	ine kinase; ss.	Bacterially expressed kinase: CFS-1:	3'mbek - a bek probe.		21-MAY-1992 (first entry)	AAQ23618;		AAQ23618 standard; DNA; 32 BP.	RESULT 1 AAQ23618/c

Result No.

C à a a

New fibroblast growth factor receptor proteins - useful in treating gf-mediated conditions e.g. angiogenesis of tumours,

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RESULT 2
AAT63287/c
ID AAT63287 standard;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prain sicm library as it is complementary to the 3' end of the partial murine bak codding sequence (Koribluth et al., Wol. Cell Biol. 8: 541-5544 1989). The fragment obtd was amplified by BekMA (AAO23619) and BekIB (AAO23620) primers, and the obtd. Kull Length bek clone was subs-equently sequenced and the protein sequence deduced. Receptor proteins encoded by this coMA sequence may be used in pharmaceutical compans. to inhibit undesirable heparin-binding growth factor mediated cellular responses or to inhibit the binding of an opportunistic particular in the sequence of the sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cornes proliferation; in vivo; hepatocyte growth factor; injury; PCR; keratinocyte growth factor; ocular surgery; epithelium; endothelium; expression; receptor; polymerase chain reaction; amplification; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The oligonucleotide 3'mbek was used screen a one day old human brain stem library as it is complementary to the 3' end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 25; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitogenic effects in psoriasis, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe for amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT63287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2708 ATCCACACATAAACGGCAGTGTTAAAACATGA 2739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drugs. See also AAQ21003,4 and AAQ23610-7.
                                                         The invention relates to methods for promoting corneal cell proliferation in vivo by treating the cells with hepatocyte growth factor (HGF) and optionally keratinocyte growth factor (KGF). Methods for suppressing corneal cell growth include administring Calons to the
                                                                                                                                                                                                                                                                                                                                                                                                                              Promoting or suppressing corneal cell proliferation - using hepanocyte growth factor or calcium lons resp. e.g. for treating corneal injury or for preserving corneal tissue prior to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5589451-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAY-1997
                                                                                                                                                                                                                                                                                              Example 1; Column 11-12;
                                                                                                                                                                                                                                                                                                                                                                                              transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        healing; beta-actin; upstream; downstream; intron; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1997-076878/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCACACATAAACGGCAGTGTTAAAACATGA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
The methods are used for the treatment of corneal tissue injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 BP; 6 A; 5 C; 7 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9208-0947683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9205-0947683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment of FGF receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
                                                                                                                                                                                                                                                                                                     25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                   following accidental injury, ocular surgery or due to corneal disorders caused by abnormal healing processes of the corneal epithelium and endothelium. The methods are based on the discovery that corneal tissue can express mRNA for HGF, KGF and their respective receptors. The discovery was shown by PGR amplification using the primers AMT63273-87. This probe is used to detect the 205 bp fragment amplified from the fibroblast growth factor (FGF) receptor 2 CDNA by primers AMT63283 and AMT63286. The probe corresponds to nucleotides 30-59 of the FGF receptor
                                                                                                                                                                                                                               1242 GATTGAGGTTCTCTATATTCGGAATGTAAC 1271
  01-MAY-1998
                                              AAV05503;
                                                                                 AAV05503 standard;
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 gene.
                                                                                                                                                                                         30 GATTGAGGTTCTCTATATTCGGAATGTAAC
                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                       30; Conserv
                                                                                                                                                                                                                                                                                                                                                           30
                                                                                                                                                                                                                                                                                                                                                           BP;
(first entry)
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                           11 A; 7 C; 4 G; 8 T; 0 other;
                                                                                    DNA;
                                                                                                                                                                                                                                                                                               0.7%;
                                                                                    30
                                                                                      ВР
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Pred. No.
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                            DB 18;
8.7e+02;
                                                                                                                                                                                                                                                                                                                   Length 30
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hepatocyte growth factor: HGF; keratinocyte growth factor;
dry eye: keratoconjunctivitis acca; probe; receptor;
fibroblast growth factor; FGF; ss.
                                                                                                                                                                                 Probe for FGF receptor DNA
                                                                                                                                                   Synthetic
                                                                                                                                                                        Inhibition;
                                                                                                                                                                       corneal epithelial cell; differentiation; treatment:
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US5703047-A 09-MAR-1995; 30-DEC-1997 Homo sapiens 95US-0400323.

21-SEP-1992; (TEXA ) UNIV TEXAS SYSTEM 95US-0400323. 92US-0947683.

09-MAR-1995;

Wilson

WPI; 1998-076459/07

Inhibition of corneal cell differentiation - by using hepatocyte
growth factor and/or keratinocyte growth factor

Example 1; Columns 17-18; 36pp; English.

The present sequence was used in the development of a novel method for the inhibition of corneal epithelial cell differentiation. The mathod comprises contacting the cells with a hepatocyte growth factor (REF) and/or kertinocyte growth factor (REF) and/or kertinocyte growth factor (REF) and/or kertinocyte growth factor (REF) and a timed sequentially or simultaneously. The HEF and/or KEF is in a timed release delivery system, especially comprising blodegradable polymen microcopsules. The HEF and/or KEF are administered optionally. The method is used for treating dry eye, especially keratoconjunctivitis sicca.

Sequence 30 BP; 11 A; 7 C; 4 G; 8 T; 0 other;

Score 30; DB 19; Length 30

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ce The present invention relates to oligonucleotides encoding polymorphic variants of protelins related to amylases, amyloid proteins, anglopoistin, components related proteins, cadherin, cyclin, polymerase, anglopoistin, cyclory stransfer, cyclin, polymerase, anglopoistin, cyclin, polymerase, anglopoistin, cyclin, polymerase, anglopoistin, cyclin, cyclin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
AAL29297
                                                Query Match
Best Local S
Matches 31
                                                                                                                                                                                 Sequence 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2100; 4143pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-1999; 99US-0173419
27-DEC-2000; 2000US-0173419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunosuppressive; immunostimulatory, antiinilammatory; cytostatic; neuroprotective; antimotroblai; gene therapy vaccine; amylade protein; angiopoletin; epoptsis related protein; cadherin; cytlin; polymerise; onogene; histone; kinse; colony stimulating factor; complement related protein; cytochome; kinses; cytokine; interferon; interfeakh; cytochome; complement calated protein; cytochome; kinses; cytokine; interferon; interfeakh; cytochome; complement calated protein; cytochome; kinses; cytokine; interferon; multifactorial disease; autolmmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-465210/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-2000; 2000WO-US35498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nervous system disease; ss.
                                   0.6%;
Local Similarity 79.5%;
hes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human SNP oligonucleotide #2505.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30
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30; Conserv
                                                                                                                                                                            BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                            7 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; 1
                                                                                                                                                               17 C; 14 G; 12 T; 0 other;
                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                      Pred.
                                                                               Score 26.2;
Pred. No. 1
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                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                      Le+04;
                                                                                                     DB 22;
                                            8;
                                                                                                     Length
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                     50;
                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                   Gaps
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                                   0;
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RESULT 6
ANK6634
ID ABK6634
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AAQ13309/c
ID AAQ13309 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
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                                                              US6352829-B1
                                                                                                                       HOMO Sapiens
                                                                                                                                                                                     Primer; ss;
                                                                                                                                                                                                                                               Human gene specific PCR primer
                                                                                                                                                                                                                                                                                                        02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                               ABK 66343;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK66343 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2488 TGTTGGCATGCAGTGCCCTCCCAGAGACC 2516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30 BP; 5 A; 8 C; 11 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The probe was used to screen a human placental lambda gtl1 library for the gene encoding basic RGF receptor. It was of from the partial cDMx clone published by Ruta et al, 1988. See also AA013308-Q13311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Extracellular form of human fibroblast growth factor receptor used to treat tumours, abnormal angiogenesis e.g. diabetic retinopathy, rheumatoid arthritis and arteriosclerosis and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 11; 29pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contraceptives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-252611/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bergonzoni L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FARM ) FARMITALIA C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe OAB984 for bFGF receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
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                                                                                                                                                                        microarray; differential expression analysis; human
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Pred. No. 9.6e+03;
                                                                                                                                                                                                                                               #431.
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ID ABK66344 standard; DNA; 25 BP
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between several different physiological sources, where the method comprises producing subpopulation of labsiet Ms for each object to physiological sources, comprising the population of appetitum specific produces to its preferably performed by appetitum specific produces the comparison associated with the surface of as subsequenting the patterns for each of the sources to asset to obscibe Ms study performed the sources to asset to obscibe Ms study as the pattern for each of the sources as subsequenting the patterns for each of the sources, where differential sources are produces a hybridisation secured in differential sources, and appearing the patterns for each of the sources where differential sources are patterns for each of the sources are produced by the formation of the sources of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to producing a sub-population of labeled nucleic acids (NAS) comprising contacting a NA sample from a physiological source, with a pool acid of 50 distinct gene specific primers under suitable conditions to enzypatation in the production of the substitution of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA, and each labeled NA is generated using a single gene specific prime. The method is useful for producing a sub-repulation of labeled NAs which is useful for analysing the differences in the RNA profiles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form of the printed specification, but was obtained in elfformat directly from USPTO at
05-JAN-1999;
                                                                                                                                                                                                                                                                                                   Primer; ss; DNA
                                                                                                                                                                                                                                                                                                                                                                             Human gene specific PCR primer
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25; Conserv
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99US-0225928
                                                                                                                                                                                                                                                                                                        microarray; differential expression analysis; human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       #432.
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1179 GCCCGACGGGCTGCCCTACCTCAAG 1203

GCCCGACGGGCTGCCCTACCTCAAG

Query Match
Best Local Similarity
Matches 25; Conserv

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0 Score 25; Pred. No. Mismatches

0.6%;

DB 24; 1.4e+04;

Length 25 Indels

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Sequence

http.wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1

25 BP; 3 A; 7 C; 11 G; 4 T; 0 other;

24-JUN-1999 WO9931267-A1 Synthetic biological sample characterisation; infectious disease; inflammatory disautoimmune disease; central nervous

central nervous system disorder;

haracterisation; diagnosis; diabetes; heart disease; inflammatory disease; neoplastic disorder;

gs.

Oligomer used in DNA obstruction assay.

AAX84630;

16-SEP-1999

(first entry)

AAX84630 standard; DNA; 42

DNA obstruction assay; receptor interaction; ligand interaction;

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The invention relates to producing a sub-population of labeled nucleic cacids (NAS) comprising contracting a NA sample from a physiological cacids (NAS) comprising contracting a NA sample from a physiological cacids (NAS) comprising contacting a NA sample from a physiological cacids (NAS) comprising the population of NAS, where cachignes specific primer has a sequence complementary to a distinct many and each labeled NA is generated using a single gene specific CC mRNA, and each labeled NA is generated using a single gene specific CC primer. The method is useful for ronalysing the differences in the RNA profiles between several different physiological sources, where the method CC comprises producing subpopulation of labeled NAS for each physiological corres, comprising the population, where the comparison comprises producing subpopulation of labeled NAS for each of the physiological sources, comprising the population, where the comparison comprises producing subpopulation of labeled NAS for each of the sources, comprising the population, where the comparison control of the sources, comprising the population, what stably concept to identify differences in the population, what stably concept to identify differences in the population, what stably concept the sources, where differential gene expression assays are utilised in differential expression analysis of diseased a normal cutisue cy, neoplastic a normal tissue, or different tissue or subtissue types. The present sequence is a human gene specific PCR primer used in the method of the invention.

Note: The sequence data for this patent did not form part of the patent directly from USPTO at human security and account of the patent of the necture of the patent o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     producting sub-population of labeled nucleic acids, useful for analysing differences in RNA profiles between several different physiological sources, using set of distinct gene specific primers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents an oligonucleotide used to test a DNA controlled usassy for assessing interaction between receptors and colligings. The invention relates to a method for the characterisation of biological samples; and comprises detecting the binding of individual members of a library of molecular probes to molecular components in the sample. The method comprises: (a) contacting the sample with a library of molecular probes to allow them to bind to their specific binding of the conjugation of molecular probes to molecular components in the sample using a bibrary of molecular probes to molecular components in the sample using a conjugation of molecular probes to molecular components in the sample to the conjugation of molecular probes to molecular components in the sample. The method can be used for characterising biological samples for the method can be used for characterising biological samples for conjugation be used for characteristic bidder to the sample conjugation of the sample molecular component such as probeins, glycoproteins, polymucleotides, can be used for characteristic bidder to a patient and for conjugation to describe a diagnosting a disease or condition in a patient and for constitution such as diabetes, infectious disease, inflammatory disease, heart disease, neplastic disorders, autoimmune disease and xx
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local s
Matches 31
               WPI; 1992-056827/07
                                     Dionne CA,
                                                          (RORE ) RORER
                                                                                                      03-JUL-1991;
                                                                                                                                                 W09200999-A
                                                                                                                                                                       Synthetic
                                                                                                                                                                                                  Bacterially expressed kinase; CFS-1; amplification:
                                                                                                                                                                                                                                                                                                                                                                       23-JAN-1992
                                                                                                                                                                                             PGDF; tyrosine kinase; ss.
                                                                                                                                                                                                                            Bek4A - a PCR primer.
                                                                                                                                                                                                                                                     21-MAY-1992
                                                                                                                                                                                                                                                                           AAQ23619
                                                                                                                                                                                                                                                                                            AAQ23619 standard; DNA; 45 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Simultaneous identification of novel biological targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 53; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SEPR-) SEPRACOR INC
                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heeiner DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                         42 BP; 32 A; 2 C; 2 G; 6 T; 0 other;
                                    Crumley G,
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                (first entry)
                                                          INT HOLDINGS.
                                                                                9005-0549587
                                                                                                     91WO-US04745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0068035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US26894
                                                                                                                                                                                                                                                                                                                                                                                                           75.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones SW,
                                  Jaye MC,
                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zepp CM.
                                 Schlessinger J.
                                                                                                                                                                                                                                                                                                                                                                                                           1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 42;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                 WPI; 2001-465210/50
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RESULT 10
AAL29254/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The oligonuclectide 3'mbek (AAQ23618)was used screen a one day old human brain stem library as it is complementary to the 3' end of the partial murine bek cooling sequence (Kornbluth et al., Mol. cell Biol. 8: 541-5544 1988). The fragment obtd. was amplified by BekAA and BekIB (AAQ23620) primers, and the obtd. was amplified by BekAA and cell biol. 9: 641-654 1988. The fragment obtd. was amplified by BekAA and cell biol. 9: 641-654 1989. The fragment obtd. was amplified by BekAA and cell biol. 9: 641-654 1989. The sequence deduced. Receptor proteins cell biol. 9: 641-654 1989. The sequence may be used in platmaceutical compans. to inhibit undesirable heparin-binding growth factor mediated cellular responses or to inhibit the binding of an opportunistic pathogen to human cells. Such undesirable responses may be growth factor stimulated consideration. Such undesirable responses may be growth factor stimulated consideration. The derived bek protein may also be used for screening drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                       28-DEC-1999; 99US-0173419
27-DEC-2000; 2000US-0173419
                                                                                                                                                                                                                                                                                                                                                                  28-DEC-2000; 2000WO-US35498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunosuppressive; immunostimulatory, entiinflammatory; cytostatic; neuroprotective; antinicrobial, spent barapy twochne; amylas cancer; amyloid protein; ampiopoletin, spentosis related protein; codherin; cytostin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytostnome; kinase; cytostne; interfero; interferor; complement related protein; cytostnome; kinase; cytostne; interferor; interf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W0200147944-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nervous system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human SNP oligonucleotide #2462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAL29254 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45 BP; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 25; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitogenic effects in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fibroblast growth factor receptor proteins - useful in treating gf_mediated conditions e.g. angiogenesis of tumous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR20750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 ACCATGGTCAGCTGGGGTCGTTTCA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 ACCATGGTCAGCTGGGGTCGTTTCA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 25; Conserv
       RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%;
ilarity 100.0%;
Conservative
Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; .11 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conditions e.g. angiogenesis of tumours, psoriasis, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 11
AAI30470
ID AAI30
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 2088; 4143pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human single nucleotide polymorphism (SNP) FGFR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI30470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI30470 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49 BP; 3 A; 3 C; 4 G; 39 T; 0 other;
                                                            Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; resequence; genotype; disease; forensic; paternity testing;
single nucleotide polymorphism; SNP; ss.
                      Claim 1; Page
                                                                                                                                                                                                                              Cargill M,
                                                                                                                                                                                                                                                                                                                       07-MAR-2000;
22-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                          07-MAR-2001; 2001WO-US07268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200166800-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                  WPI; 2001-522952/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                       ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 72.7
32; Conservative
                                                                                                                                                                                                                           Ireland
                                                                                                                                                                                                                                                                                                                    2000US-0187510
2000US-0206129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                      87; 145pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
replace(16,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.68;
                                                                                                                                                                                                                              JS,
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                                                                                                                                                                                                                              Lander ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΒF
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Pred. No. 2.2e+0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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The invention relates to the identification of nucleic acid molecules (AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. containing the polymorphic sites may be useful in forensics and paternity
testing.
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Sequence 31 BP; 3 A; 13 C; 12

G; 3

T; 0 other;

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Matches
                                                  Query Match
                1034 ACCGGCCCATCCTCCAAGCCGGACTGCCGGC 1064
                                  Local Similarity
nes 27; Conserv
۳
ACCGGCCCATCCTGCAGGCGGGGCTGCCGGC
                                  Conservative
                                           0.6%;
                                   0
                                           Pred.
                                                     Score 24.6;
                                    Mismatches
                                             ŏ.
  3
                                            .9e+04
                                                      DB
                                                     22;
                                                     Length
                                      Indels
                                                      31;
                                      0
                                      Gaps
                                      0;
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밁 S

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02-FEB-2001
                                                                                                       AAA98316 standard; DNA;
Human MSH6 fragment 8/exon 8 to 10 DNA Ref-Seq fragment
                                    (first entry)
                                                                                                       50
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neoplastic disease; drug development; ds mutation; carcinoma; colorectal; endometrial; Human mismatch repair gene; hMSH6; disease predisposition; genotype; ovarian; leukemia;

Homo sapiens.

DE19909878-A1

07-SEP-2000

06-MAR-1999; 99DE-1009878

06-MAR-1999; 99DE-1009878

(UYDR ) UNIV DRESDEN TECH

WPI; 2000-588378/56.

Plaschke J,

Kruppa C,

Schackert H;

determining predisposition to cancer and for development of drugs Novel variants of the human mismatch repair gene, MSH6, useful e.g. for

Disclosure; Fig 3; 14pp; German.

This invention describes a novel method of determining a predisposition cc to disease by genotyping a subject's DNA sequence (A) of the human cc mismatch repair gene, MSHG at specified positions and comparing with creference DNA sequences, optionally taking into account all possible combinations of variations of the individual mutations. Including any chosen absolute number of variations. (A), and analysis of their combinations of relations in Following: (1) determining a predisposition of the disease, especially colorectal, endometrial and overlan carcinoma and to disease, especially colorectal, endometrial and overlan carcinoma and clukenia; (ii) determining an increased mutation rate (frequency of base substitutions, insertions and/or deterions) in subaryotic cells; (iii) copplastic disease; (iv) the development of therspectic and 'life-sayle' complastic disease; (iv) the development of therspectic and 'life-sayle' complastic disease; (iv) the development of therspectic and 'life-sayle' complastic disease; (iv) the development of therspectic and 'life-sayle' complastic (vi) optimizing individual treatments and interventions against complastic (vii) controlling the mutation rate in enkaryotic cells, in vitro or in vivo; (viii) constructing genes and vectors, particularly for

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Query Match
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                                                                        used in the method of the invention. The invention provides a new solid support for the immobilisation of nucleotide sequences. The support molecule is a diol linked to a controlled pore glass particle (CREP), by a phosphodiester bond. Oligonucleotides can then be linked to the diol, by linkage to the free hydroxyl groups of the diols. A protected nucleotide segment can then be linked to the diol-linked oligonucleotide by tandem ligation. This method can also be used as a continuous source by tandem ligation.
by tandem ligation. This method can also be used as a continuous source of supply for pre-determined, frequently used oligonucleotides, such as universal primers and diagnostic probes. The immobilized sequences can be used for e.g. gene detection, diagnostic assays, priming of enzymatic
                                                                                                                                                                                                                                The sequences represented by AAT05795 and AAT05796 are oligonucleotides used in the method of the invention. The invention provides a new solid
                                                                                                                                                                                                                                                                                                                                                           New support for immobilising nucleotide sequences - comprising controlled pore glass particles, phospho:di:ester linkage and o
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-320874/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Georges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEOR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA1336690-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      development of pharmaceuticals; (ix) developing diagnostic kits and other systems for genotyping; and (x) developing in vivo and in vitro test systems for expressing individual forms of the MSH gene, e.g. for studying pathophysiology of disease or processes in which MSH6 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diol linked oligonucleotide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT05796 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAACAAAAAACTTTTTTTTTTTTTTTTAATTTTAAGGGAAGTTT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEORGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 BP; 17 A; 4 C; 5 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA synthesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                solid support; diol; controlled pore glass particle; CPGP; primer; diagnostic probe; gene detection; diagnostic assay;
                                                                                                                                                                                                                                                                                                                       Fig 1c; 23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89CA-2615014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89CA-2615014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug development and testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.6%;
70.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "I linked to controlled pore glass particle via a new linkage consisting of 1,5 pentanediol or 1,7 heptanediol and a phosphodiester bond, as follows p-O-P(O)(O-)-O-(CH2)nO- where p is the controlled pore glass particle and n is 5 or 7"
                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΒP
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No. 2
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Or this invention describes a novel method for obtaining a set of the bialistic markers represented in ANX3233-X25622 and ANX22833-X25843 for use in constructing a high density equilibrium map of the human genome. The method involves (a) obtaining a nucleic acid library comprising CC genomic DNA fragments comprising the full genome or a portion of the method involves (a) obtaining a nucleic acid library comprising CC (b) determining the order of genomic DNA fragments of the genomic DNA fragments and (d) identifying nucleotides in the genomic DNA fragments (c) determining the sequence of selected regions of the genomic DNA fragments and (d) identifying nucleotides in the genomic DNA fragments which vary between individuals, thereby defining a set of bialislic CC markers, the methods can be used for identifying traits such as disease. CC (e.g., Alzabelmer's disease, of the genome (preferably the human genome). The sequences described in a genome (preferably the human genome). The sequences described in a from the interval of the preferably the human genome of the processor of the method of the processor of the processor of the method of the processor of the proce
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Production of biallelic markers - by obtaining a genomic DNA
library, determining the order and sequence of DNA fragments
identifying nucleotides which vary between individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 130;
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18-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biallelic marker; human; high density disequilibrium map; disease; trait; identification; Alzheimer's disease; drug response; drug ef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug toxicity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNN synthesis, isolation and purification of DNN binding proteins. The advantage with this method is that the sequences can be supported to the control of the protected simply by using a solution of Naou, whereby the oligonucleotides remain attached to the solid phase and the integrity of the nucleotide strand is unaffected. This method is also faster and more efficient than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9904038-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX52549 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 42 BP; 5 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0082614.
97EP-0401740.
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                                                                                                                                                                                                                                                                                                                                                                                                                          288pp; English.
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Pred. No. 2
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                                                                                                                                                                               ANZ6554 to ANX6979 represent human biallelic markers from the present invention; which contain a polymorphic base at position 24 of their nucleotide sequences. ANZ69579 to ANZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses; they can be used for high density mapping of the human genome, and in complex association studies and haphotyping studies which are useful in determining the genetic basis for disease studies which are useful in determining the penetic basis of disease states, compositions and methods of the invention can also be useful for the identification of the torques for the development of pharmaceutical agents and disgnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents agents acting on a disease as well as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ66994 standard; DNA; 47 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel biallelic markers used to construct a high density disequilibrium map of the human genome \,\,\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-013267/01.
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23-NOV-1998;
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                                                                                       N.B. The SBQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing
                                                                                                                                                         creatment.
                                                                 from the present invention
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Local Similarity 78.4%;
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98US-0109732
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Query Match Best Local Similarity

0.6%; 78.4%;

Score 24.2; DB 21; Pred. No. 3e+04;

Length 47;

Sequence 47 BP; 17

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AGAGATGGAAAAAAACGTAGGCCTTCTGGGTAAATGG
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Search completed: December 11, 2002, 17:45:48 Job time : 557 secs

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Database
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1660 9 1579 0 1555 0 1555 1 14 1 1367 1 1330	222222222222222222222222222222222222222	Result
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9 AF487553 10 RRFIEGFC 10 RRFIEGFC 10 RRFIEGFB 5 PWFGFR2 5 NVILPGFR 5 ARRO07135 5 ARRO07135 6 ARRO07167	DB ID    AN31911	SOMMAKLES
	Description  AX33811 Sequence AX338117 Sequence AX338127 Sequence AX33622 Sequence AX3622 Sequence AX3622 Sequence AX3622 Sequence AX3623 Human bek m 26960 H. Saptens f 27960 H. Saptens f 2799	

TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX332811	RESULT 1
Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D. R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1	Homo sapiens	human.	•	AX332811.1 GI:18123445	AX332811	3320 from Patent WO0194629	AX332811 4268 bp DNA linear PAT 09-Jan-2002		

ALIGNMENTS

TAAGCAGGAGCATCGCATTGGAGGCTACAAGGT	GTGGCTGAAAAACG
GGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTA	1 CGGTGGCTGAAAACG
	Db 781 CCTGCGGCCAACACTGT
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	721 AACAAGAGAGCAC
GACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAAC 7	O-
GACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAAC 7	Qy 661 TCCGGAGATGATGAGGATGACACCGATGGTG
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SAGTCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCGCCGTG 4	Db 421 TACGTGGCTGCGCCAGGGGAGTCGCTAGAGGTGC
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	JOURNAL patent: WO 01946 Avalon Pharmaceu FEATURES Locatio Source /organia
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192	CTGGTGTCAGAGATGAGATGATGAAGATTGGGAAACACAAGAATATCATA	00	Дb
r 1920	GATCTGGTGTCAGAGATGGAGATGAATGATGGGAAACACAGAATATCATAAAT	1861	Οy
1860	GTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACCTTTC	œ	Db
1860	AGGCGGTCACCGTGGCCGTGAAGATGTTGAAAG	1801	Qy
180	GGTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCAAG		Db 5
180	CTTTCCTTTTCGCCAACTCCATGCCGCAAGCACTGGGGAATTGACAAAGACAAGCCCCAA	74	2 !
1740	GAGGACCCAAAATGGGAGTITICCAACAGATIAAGCTGACACCIGGGCAAACCCCCTGGGAGAAATGGGAGTITICCAACAGATIAAGCTGACACCTTGGGCAAGCCCCTGGGGAGAAAGCCCCTGGGGAGAAAAGCCCCTGGGGAGAAAAGCCCCTGGGGAGAAAAGCCTGACACTGGGCAAAACCCCCTGGGGAGAAAAGCCTGACACTGGGCAAAACCCCCTGGGGAGAAAAGCCTGACACTGGGCAAAACCTGGGAGAAAAGCCTGACACTGGGCAAAACCCCCTGGGGAGAAAAGCCTGACACTGACACTGGGCAAAACCCCCTGGGGAGAAAAGCCTGACACTGACACTGACACCTGGGCAAAACCCCCTGGGGAGAAAAGCCCCCTGGGGAGAAAAGCCCCCTGGGAGAAAAAGCCTGAAAAAAGCTGAACACTGAAAAACCCCCTGGGGAGAAAAAGCCTGAAAAAGCCTGAAAAACCCCCTGGGAAAAAAGCCTGAAAAAAGCTGAACACTGAAAACCCCCTGGGGAAAAAAGCCTGAAAAAAGCTGAACACTGAAAAACCCCCTGAAAAACACAAAAAAAA	1681	Db Qy
168	GCCTCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCC	62	ф
168	CGCCTCTCTAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGAAGTATGAACTTCCA	Ö	δ
1620	TTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAAC	1561	рь
1620	GTTTCGGCTGAGGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA	1561	Qy
1560	AGCAGCCAGCCGGCTGTGCACAAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAACA	50	DЬ
1560	GCAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCCTGCGGAGACAGGTAAC	U1	δò
: 1500	TGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTC	-	밁
: 1500	GTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTT	•	Qy
: 1440	유=	1381	Db
: 1440	AGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATC	1381	Q
1380	ATATCCTTTCACTCTGCATGGCTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATT	1321	망
1380	TATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAG	N	ρ
1320	TGG	1261	Db
1320	GGAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTG	1261	ν.
1260	TCTCTATA	N	DЬ
1260	GGTTCTCAAGGCCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTCTAT	1201	Qy
1200	TGGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTC	-	Db
1200	GGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCT	1141	Qy
1140	GATGCCCAGCCCCACATCCA	1081	Dр
1140	TCGGAGGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCC	1081	Qy
1080	CCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGT	1021	DЬ
1080	AGCGATCGCCTCACCGGCCCATCCTCCAAGCCGGAC	1021	οy
1020	TGGATGTTGT	961	В
1020	CCTGTGTGGGGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGT	961	Qγ
960	GAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATT	901	Db
960	GAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATT	901	Qy
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GTCCATCTT	CATAGAAAATTGAAACACAGAGTTGTTCTGCTGATAGTTTTGGGGATA	3901	Qy	
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TCAAGTCCCA 39	TTGATAATGGCTTCCAGACTCTTTGCGTTGGAGACGCCTGTTAGGATC	3841	Qγ	
80 .	GCTGGCCTTCTGCTCTGAGTTGCACATTAATCAGATTAGCCCTGATTCTC	3781	Db	
TTCAGTGAAT 38	CTGGCCTTCTGCTTCTGAGTTGCACATTAATCAGATTAGCCTGATTCT		Оу	
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		60	Db	
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TTCACCGAGCA 3	TTTTAATAGCTATTTGCTAAATGCTGTTCTTACACATAATTTCTTAATT	3241	Ф	
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rese 540	ATCAGTTGGACTAAGGATGGGGTGCACTTGGGGGCCCAACAATAGGACAGTGCTTATT	4	9
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AGTG 420 AGTG 420	GATACCACATTACAGCCACAAGAGCCACCAACTACCACATACCTCTCACCCAACTACTGCTCAACCAAC	361	B 8
. 3 36	CTGGTCGTGGCACCATGGCAACCTTGTGCCTGGCCCGGCCCTCCTTCAGTTTAGTTGAG		B 8
77GC 300 27GC 300	TATIGGAAGAGGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGC	241	B 8
JAGA 240       JAGA 240	TTGCCCCTAGTCCATCCCCTAGAGGAAGTGTCGAGTGGAGTAGAACGTCCACATGGACATTGCACATGGACATGGAATGGAATGGAATGAACGTCCACATGGAGAAGTGGCATTAACGTCCACATGGAGAAGTGGCATTAACGTCCACATGGAGAA	181	8 8
GCA 180      GCA 180	AAGTAACTGCAGCAGCAGGGGAGCGCTCGGTTCCTGAGCCCACGGCAGGTGAAGGCAAGGGAGTGAAGGCAGTGAAGGCAGGAGGAGGAGGAGGGGCTGGAGGGAG	121	D 04
NTC 120	TCCATCCCGACCCACCCGGGGGGGGGACAACACAGGTCGCGGAGGAGGGTCGCTATTC TCCATCCCGACCCACCCACGGGGGGGGGACAACACAGGTCGCGGAGGAGGGTTGCCATTC TCCATCCCGACCCACGGGGGGGGGG	61	B 6
TTC 60	CCCAAGGACCACTCTTCTGCGTTTGGAGTTGCTCCCCACAACCCCGGGGCTCGTCGTTTTCCCCACGACACCACGGCCCCGGCTCGTCGCTTTCCCCCACACACCCCGGGCTCGTCGTCTTTCTCCCCACACACCCCGGGCTCGTCGTCTTTCTCTCCCACACACCCCGGGCTCGTCGTCGTTTCCCCACACACCCCGGGCTCGTCGTCGTTTCTCTCTC	<b>-</b> -	B 6
Gaps 0;	tech 100.0%; Score 4268; DB 6; Length 4268; Da 1 Similarity 100.0%; Fred, No. 0; A 100.0%; Pred, No. 0; Indels 0; A 100.0%; Conservative 0; Mismatches 0; Indels 0;	Query Match Best Local Matches 426	
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eleostomi; mo. ,G.,	human sepiens  Homo sepiens  Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eut  Mammalia: Euthoria: Primates: Catarrhini; Hominidae: Ho  Young.Pa. S., Sopper.D. R. and Weaver.Z.  Horioan S., Sopper.D. R. and Weaver.Z.	ORGANISM ORGANISM FERENCE AUTHORS	RE SO
09-JAN-2002	AX334117 AX334117. GI:18124836	RESULT 2 AX334117 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS	K E C E C E C E C
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AAA 4260     AAA 4260	ATGTTTCTACAGATATTAATGTTAACAAGACAAAATAAAT	4201 .	9 9
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GTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA 1620
                                                                              CGGAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGG
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٠ ٦	1621 1621	COCCTCTCTTCAACGGCACACACCCCCATGCTGGCAGGGGTCTCGGAGTATGAACTTCCA	1680
•	1681	GAGAA        GAGAA	1740 1740
• •	1741 1741	CCAAG CCAAG	0 0
• •	1801 1801	TTCT	œ œ
•	1861 1861	4-4	1920
	1921 1921		1980
	1981 1981		2040
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	2101 2101	CTGCCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGGC 2 	2160
	2161 2161	AGAANTGTTTTGGTANCAGANACANTGTGATGANATAGCAGACTTTGGACTCGCCAGA 2	2220
	2221 2221	GATATCAACAATTAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGG 2	2280
	2281 2281	#TGGCTCCAGAAGCCCTGTTTGGTAGAGTATACAGTCATGAGTGATGTGTGGTCCTTC 2	2340
	2341 2341	GGGGTGTPAATGTGGGAGATCTTCACTTTAGGGGCTCCCCTACCCAGGATTCCCGTG 2	2400
	2401 2401	GARGAACTTTTTAACCTCCTGAAGGAAGGACCAGAATGGATAAGCCAGCC	2460
	2461 2461	AACGAACTGTACATGATGATGATGAGGACCTGTTGGCATGCAGTGCCCTCCCAGAGACCAAGG 2	1520 1520
	2521 2521	TTCAAGCAGTTGGTAGAAGAGTTGGATTGGATTCTGAGTGTCAGAGCAATGAGGAATAG 2	580
	2581 2581	TTGGACCTCAGCCACCTCTGGAAAGATTTCACCTAGTTACCCTGACACAGAAGTTCT 2	640
	2641 2641	TOTTCTTCAGGAGATGATTCTGTTTTTTCTCCGGAGCCCATGCCTTACGAACCATGCCTT 2	700

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3720 3720	CANCOTCTAACTGGACTTCCCAAGATAAATGGTACCAGGGTCCTCTTAAAAGATGCCTTA		Db 99
3660 3660	AGAACTCATTCATAGGAAGGTGTTCATTTGGTGCGACCCCTGTCATTACGTCAGG 	3601	Оу
3600	GTGTTTAAATGCTGCTGCAGACGATTGTTCTTAGACCTCCTAAATGCCCCATATTAA		Db Qy
3540 3540	AAAGGAATATTTACAATTTATGACTAATTTGGGGAAAATGAAGTTTTGATTTAT 	481	} B &
3480 3480	(AGCAGACTASTTARTCATTGCTTGGACTTAACTAGTTATCAGATCC	421	}
3420 3420	GGTAATATACAAAACAATTAATCATTTATAGTTTTTTTTGTAATTTAAGTGGCATTTCT 	36	Db Oy
3360 3360	ISIGAAAAATACTTTTGCTTTCAGGGAAANTGGTATAACCTTAATTTATTAATAAAT 		D 49
3300	I HARIAGCIATTIGCTAAATGCTGTTCTTACACATATTCTTAATTTTCACCGATATTTTTCACCGATATTTTCACCGATATTTTCACCGATATTTCACTAAATTTTCACCGATATTTCTTAATTCTTAATTTTCACCGATACTTCTTAATTTTCACCGATACTTAATTTCACCGATACTTCTTAATTTTCACCGATACTTAATTTCACCGATACTACTCTTAATTTTCACCGATACTTAATTTTCACCGATACTTAATTTTCACCGATACTACTCTTAATTTTCACCGATACTTAATTTTCACCGATACTACTCTTAATTTTCACCGATACTACTCTTAATTTTCACCGATACTACTCTTAATTTTCACCGATACTACTCTTAATTTTCACCGATACTACTACTACTACTACTACTACTACTACTACTACTAC		p 4
3240 3240	TTTTGTATTCATTTAAATGGATGTCCCAATGCACCTAGAAAATTGGTCTCTCTTT	3181	P 9
3180	GGATGTAT	12 12	Db Qy
3120 3120	AATTGGAGAAGATTTATGTO                  AATTGGAGAAGATTTATGTO	90	Db Qy
3060	CTGTGGACCAGTAGGACTCA               CTGTGGACCAGTAGGACTCA	0 0	Db Oy
3000	GGAGCAGTGGACTGCC.               GGAGCAGTGGACTGCC.	9 9	Db Qy
2940 2940	TGTGTAAAGATTTATACAGTTGAAAA 	<b>80 80</b>	Оу
2880 2880	TTGTTGTCTCCACTTGTATNTATGGATCAGAGGAGTAAATAATTGGAAAAGTAATCAGCA		Оy
2820 2820	CAMCAGGACACACTGGGAMCTMGCTMCACTGAGCAGGGAGACCATGCCTCCCAGAGC	2761 2761	Оy
2760 2760	CCTCAGTATCCACACATAAACGGCAGTGTTAAAACATGAATGA	270J 270J	Оу

120 120	TOCATICCCACCCACCCACGCGGGGGGGACACACACACAGTTCGCGAGGAGGAGCGTTGCCATTC 	61	B 8
60	CCCAAGGACCACTCTTCTGCGTFTGGAGTTGCTCCGCACAAGGCGGGGGGGGGG	<b>-</b> -	p 6
aps 0;	tch 100.0%; Score 4268; DB 6; Length 4268; BI Similarity 100.0%; Pred. No. 0; 4268; Conservative 0; Mismatches 0; Indels 0; G	Query Ma Best Loc Matches	
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signature	Young, P.E., Augustus, M., ( Horrigan, S., Soppet, D.R. & Cancer gene determination gene sets	AUTHORS	
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4260	TIGETECHACAGATATTAATGETAACAAGACAAAATAAATGETAACAGAACTETAAAAAAAA	4201	p 9
20	TGTTACAAAATTGGACAAAGTATTTAATAAAACCTGTTAATTTTTATACTGACAATAAAA	4141	da
4200	TGTTACAAAATTGGAGAAAGTATTTAATAAAACCTGTTAATTTTTATACTGACAATAAAA	4141	γQ
4140 4140	AAACACCACTCACTTGCAATAGCGTGCAAGATGAATGCAAGTTAGACTGTTTATG	4081	ρ <del>ζ</del>
4080	TACATICAGACAAATATATGGCGGTTGTTCCTTCTGTACTAAAGTATTGTGTTTTGCTTTGG TACATICAGACAAATATGGCGGTTGTTCCTTCTGTACTAAAGTATTGTGTTTTGCTTTTGG TACATICAGACAAAATATGGCCGTTGTTCCTTCTGTACTAAAGTATTGTGTTTTGGTTTTGG	4021	95 55
4020	TAMAGGAPTGCTTTCATCTAATTCTGGCAGGACCTCACCAAAAGATCCACCCTCATACC	3961 3961	8 양
3960 3960	TCATAGAAAATTGAAACACAGAGTTGTTCTGCTGATAGTTTTGGGGATACGTCCATCTTT	3901 3901	g Qy
3900	TITGATAATGGCTTCCAGACTCTTTGCGTTGGAGACGCCTGTTAGGATCTCTAAGTCCCA	3841 3841	B 8
3840	GCTGGCCTTCTGCTTCTGAGTTGCACATTAATCAGATTAGCCTGATTCTCTTCAGTGAAT 	3781 3781	B 8

1200 1200	TGGATCAAGGACGTGGAAAAGAACGGCAGTAAATACGGGCCGGACGGCGTGCCTACCTG	1141	₽ 9
	GTCCGAGCAGACTRAAGTTTTCTCTCCAACTTTTAAGTGATTCCCCAGCCCCAACTCCACCCCACTCCACCCCACTCCACCCCACCCCCACTCCACCCCACCCCCACCCCCACCCCCACCCCCACCCCACCCC	1081	B 5
	GAGCGATCGCCTCACGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTG	1021	рb
1020 1020	ACCTGTGTGGGGGAATGAATACGGGTCCATCAATCACAGGTACCACCTGGATGTTGTG	961	윰 3
960	CGAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAGGGAAATTAT [	901	DP 6A
900	CGGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCACTGGAGGCTACAAGGAAGCTACAGAGAACTTTAAGCAGGAGCATCGCACTGGAGGCTACAAGGAAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTA	841	B 8
840	CCTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGAACCCAATGCCAACCATG	781 781	ФР
780 780	ARCANGADACCANCANATIGGACCACACAAAAAANTIGGAAAACGGGCTGCATGCTTGTG 	721 721	Db Qy
720 720	TCCGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGACAGTGATA TCCGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAAC TCCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAAC	661	Db Qy
660	AGTAGGACTGTAGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCA	601	ОУ
600	GACTACTTGCAGATAAAGGCCCCCCCCCCCCCCAAGACTCCGGCCCTTATGCTTGTATGCCCGGCCCGCCC	541 541	g 94
540	ATCAGTTGGACTAAGGATGGGGTGCACTTGGGGCCCAACAATAGGACAGTGCTTATTGGG   ATCAGTTGGACTAAGGATGGGGTGCACTTGGGGCCCAACAATAGGACAGTGCTTATTGGG   ATCAGTTGGACTAAGGATGGGGTGCACTTGGGGCCCAACAATAGGACAGTGCTTATTGGG	481	ρ <sub>0</sub>
480	TACGTGCCTGCCCAGGGGAGTCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCGCCGTG +	421 421	gg Qy
420	GATACCACATTACAGCCAGAAGACCACCACCAATACCAATTACCACTCTCAACCAGAAGGCACACGACAGAAGGCACACACA	361 361	ОУ
360	CTGGTCGTGGTCACCATGGCACCTTGTCCGTGGCCCGGCCCTCCTTCAGTTTAGTTGAG 3	301	요 성
300	TATIGANAGGANCCGGGATTGGTANCGTANCATGGTCAGCTGGGGTGGTTGCATGGT   TATIGANAGGANCCGGGATTGGTACCGTANCCATGGTCAGCTGGGGTGGTTCATCTGC 3   TATIGANAGAGGANCGGGGGTTGGTCAGCTANCCATGGTCAGCTGGGGTGGTTCATCTGC 3	241 241	P Q
240	TTECCECTACTCCATECCCCTACACAACTCTCCACATGGCATTAACCTCCACATGGCACTTACTT	181 181	P Oy
180	AAGTGACTGCAGCAGCAGCGCAGCGCACCGCCTTCGGTTCCTGAGCCCACGCCAGGCTGAAGGCA 180 	121 121	유

2340	ATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTC	2281	8
28	GATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGG	22	Db
28	ATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGG	N	QΥ
2220			DЬ
Š	AAATGTTTTGGTAACAGAAAACAATGTGATGAAAAATAGCAGACTTTTGCACTCCACA		ş
2160	CTGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCC	2101	Db 4
10	TFAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAG	• •	2 5
2100	ATTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACCTTGGTGTCATGCACCTACCAG		, Q
9	GGCAACCTCCGAGAATACCTCCGAGGCCCGGAGGCCACCCGGGATGGAGTACTCCTATGAC	9	ДĎ
2040	GGCAACCTCCGAGAATACCTCCGAGCCCGGGAGGCCACCCGGGATGGAGTACTCCTATGAC	98	Qy
1980 1980	CTTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTTAAA	1921 1921	β Q
1920	GATCTGGTGTCAGAGATGGAGATGATGAAGATGATT	m	Ф
1920	GATCTGGTGTCAGAGATGGAGGATGAATGAAGATGATTGGGAAACACACAGAATATCATAAA	98	Qy
1860	THE PROPERTY OF THE PROPERTY O	80	B 5
. 80	GETTGUTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCAAG	9 4	0 5
1800	GTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCAAG	1741	. Q
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68	CGCCTCTCTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGGAGTATGAACTTCCA	1621	B 3
1620	GTTTCGGCTGAGTCCAGCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA	in	рb
1620	GTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAAC	1.7	Q
1560	AWANGCAGCCAGCCGGCAAACCTAAACCTATCCCCCTGCCGAAACAGAACGTAACA	1501	B 3
1500	TGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTT	4 4	) B
1500	TGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTC	4	δδ
4	ACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCC	ä	Вb
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J N	1 CGGAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGG 	126	당 성
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1260	STTCTCAAGGCCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTCTATAT	120	γQ

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Homo saplens brain cDNA to mRNA.
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Matches 4268;
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Sugimura, T. and Terada M.
K-sam gene encodes secreted as well as transmembrane receptor
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TTGGACCTCAGCCAACCTCTCGAACAGTATTCACCTAGTTACCCTGACACAAGAAGTTCT 26	TTCAAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCTCACAACCAATGAGGAATAC 25	AAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCTCACAACCAATGAGGAAT		TGTACATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAAC	GAGGAACTTTTTAAGCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCC	GGCTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCTACCCAGGGATTCCCCTG 24	500		AGTGATGTCTGGTCC		ATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAC		ACTCGCCAGA 2	THE CTGGCCAGAGGCATGGAGTACTTGGCTCCCAAAAATGTATTCATCGAGATTTAGCAGCC 21	TRACCO AGA COC ATTO COTTA COTTA COTTA CONTROL A CONTROL ACT ACCORDED A CONTROL ACT ACCORDED A CONTROL ACT ACCORDED A CONTROL AC	AACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAG 2	GCAAC	HAGAATACCTCCGAGCCCGGAGGCCACCCGGGATGGAGTACTCCTAT		TTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCT	GATCTGGTGTCAGAGATGAGATGATGAAGATGATTGGGAAACACAAGAATATCATAAAT 19	ATCTGGTGTCAGAGATGGAGGATGATGAAGATTGGGGAAACACAAGAATATCATAAAT 1	GAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAAGATGATGCCACAGAGAAAAGACCTTTCT 18	GGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAAGACCTTTCT 1		GCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAAGCCCAAG 1		ACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAGAA 1		TCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCA 1		SGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA 1		COAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAAC

CAACGTCTAACTGGACTTCCCAAGATAAATGGTACCAGCGTCCTCTTAAAAGATGCCTTA	3601 AAGAACTCATTCATAGGAAGGTGTTTCATTTTGGTGTGCAACCCTGTCATTACGTCAACG 3660	3541 TIGTGTTTAAATGCTGCTGTCAGACGATTGTTGTTAGACGTGCTAAATGCCCCATATTAA 3600 11111111111111111111111111111111111	3481 TTTGANAGAGARINTTRACANTARNGACTANTTRGGGGANANTGANGTHTTTGATTTNT 3540 3481 TTTGANAGAGARINTTRACANTARNGACTANTTTGGGGANANTGANGTTTGATTTNT 3540	3421 ATGCAGGAGAGAGAGCAGTAGTTAATCTATTGCTTGGGACTTAACTAGTATTATCAGATCG 3480 3421 ATGCAGGAGCACAGCAGACTAGTTAATCTATTGCTTGGGACTTAACTAGTTATCAGATCC 3480 3421 ATGCAGGAGCACAGCAGACTAGTTAATCTATTGCTTGGGACTTAACTAGTTATCAGATCC 3480	3361 TOGTAATATAAAAAAATATTAATCATTTATAGTTTTTTTGTAATTTAAGGGCATTTCT 3420 3361 TOGTAATATACAAACAATTAATCATTTATAGTTTTTTTTGTAATTTAAGGGCATTTCT 3420 3361 TOGTAATATACAAACAATTAATCATTTATAGGTTTTTTTTGTAATTTAAGGGCATTTCT 3420	3301 GAGGTGGAAAATACTTTTGCTTTCAGGGAAAATGGTATAAGGTAATTTATTAAAT 3360 3301 GAGGTGGAAAAATACTTTTGCTTTCAGGGAAAATGGTATAAGGTTAATTTATTAATAAAT 3360	2241 TETTANTAGCTANTTGCTAAATGCTGTTCTTACACATAATTTCTTAATTTCTAACGCAGCA 3300 2241 TETTAATAGCTANTTGCTAAATGCTGTTCTTACACATAATTTCTTAATTTCACCGAGCA 3300 2241 TETTAATAGCTANTTGCTAAATGCTGTTCTTACACATAATTTCTTAATTTCACCGAGCA 3300	3181 TATTTTTTGTATTGAATTGAATGGACGCCAATGGACCTAGAAAATTGGTCTCTCTTT 3240 3181 TATTTTTTGTATTGAATTGAATTGAATGCCCCAATGGACCCTAGAAAATTGGTCTCTCTTT 3240	3121 TGGATGTAAGTATATATATATATATATATATATATATAT	TAATTGGAGAAGATTTATGTCAGCACACACTTACAGAGCACAAATGCAGTATATAGGTGC	THE	2821 TTGTTGTCTCCCCCTTGTATATATGTGATCAGAGGAGTAAATATTTUGAAAAATTATCAGCA 2000 2881 TATGTGTAAAAGTTTATACAGTTGAAAACTTGTAATCTTCCCCAGGAGGAAGAAGAAGTT 2940 111111111111111111111111111111111111	CAACAGACACCACTGGCAACCTACGCTACACTGACCAGGAGACCATGCTTCCASAAG TTGTTGTCTCCCACTTGTATATATGGATCAGGAGGATAATTGGAAAAGTAATCAGCA 	CCTOAGTATCCACACATAAACGGCAGTGTTAAAACATGAATGACTGTGTCTGCCTGTCCC CAAACAGGACAGCACTGGGAAGCTAGCTACACTGAGCAGGGAGACCATGCCCTCCCAGAGC	TGTTCTTCAGGAGATGATTCTTGTTTTTTTCTCCAGACCCCATGCCTTACGAACGA	TIGAGCCTCAGCAACCTCCCAACAATATCACCTAGTTACCCTGAACAACATCTCT TGTTCTTCAGGAAGATGATTCTTCTCCCAGACCCCATGCCTTACGAACCACGCCTT	
	PUBLISH 1697263 FEATURES Location/Qualifiers Source 1.3415		Allelande Road, King of Prussia, PA 194 2 (bases 1 to 3415) Dionne,C.A., Crumley,G., Bellot,F., Kar Rufa,M., Burgess,W.H., Jave,M. and Sch	REFERENCE 1 (bases 1 to 3415) AUTHORS DinnerC.A. AUTHORS DinnerC.A. Direct Submission JOHNAL Submission JOHNAL Submission	SOURCE HOMO SAPIANS ORGANISM HOMO SAPIANS ORGANISM HOMO SAPIANS EMBERYOTA METROCA: Chordata; Craniata; Vertebrata; Butcleostom1; Mammalia; Entheria; Primates; Cararrhini; Hominidae; Homo.	x52832 x52833.1 GI:31373 cell surface glycoprotein; fibroblast tyrosine kinase.	RESULT 5 HSPGFRHE LOOUS HSFGFRHE DEFINITION Human bek mRNA for fibroblast growth factor receptor-HEX.	4261	HITTIAN AND AND AND AND AND AND AND AND AND A	4141	Oy 4021 TACATCAGACAAATATCGCCGTTGTGTCTGTACTAAAGTATTGTGTTTTGGTTTGG 4080	QY 3961 TTAAGGATTGCTTTCATCTAATTCTGGCAGGACCTCACGAAAAGATCCACCCTCATACC 4020	Qy 3901 TCATAGAAAATTGAAACAGAGTTCTTCTCGTGATAGGTTTGGGGGATACGTCCATCTTT 3960 111111111111111111111111111111111111	Oy 3841 TITGATAATGGCTTCCAGACTCTTTGCGTTGGAGACGCCTGTTAGGATCTTCAAGTCCCA 3900	Oy 3781 GCTGGCCTTCTGGTTTGCAGTTGCAATTAATCAGATTAGCCTGATTCTCTTCAGTGAAT 3840		Db 3661 CAACGTCTAACTGGACTTCCCCAAGATAAATGGTACCAGCGTCCTCTTAAAAGATGCCTTA 3720

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539 CATGGTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGGATGACACCGATGGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 GGCCCGGCCCTCCTTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAAGAGCCACCAAC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 CATGGTCAGCTGGGGTCGTTTCATCTGCCTGGTCGTCACCATGGCAACCTTGTCCCT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 CATGGTCAGCTGGGGTCGTTTCATCTGCCTGGTCGTGGTCACCATGGCAACCTTGTCCCT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GCAGATGGGATTAACGTCCACATGGAGATATGGAAGAGGACCGGGGATTGGTACCGTAAC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213
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                                                                                    CATGGTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGGATGACACCGATGGTGC 692
                                                                                                                                                                                                                                                                                     AGACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAGACAGTGAAACTTGGTACTT 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCAACAATAGGACAGTGCTTATTGGGGAGTACTTGCAGATAAAGGGCGCCCACGCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCAACAATAGGACAGTGCTTATTGGGGAGTACTTGCAGATAAAGGGGGCCACGCCTAG 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGCTGCCTGTTGAAAGATGCCGCCGTGATCAGTTGGACTAAGGATGGGGTGCACTTGGG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGCTGCCTGTTGAAAGATGCCGCCGTGATCAGTTGGACTAAGGATGGGGTGCACTTGGG 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAATACCAAATCTCTCAACCAGAAGTGTACGTGGCTGCACCAGGGGAGTCGCTAGAGGT 358
                                                                                                                                                                                                                        AGACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAGACAGTGAAACTTGGTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGATGGGATTAACGTCCACATGGAGATATGGAAGAGGACCGGGGATTGGTACCGTAAC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCCTGAGCCCACCGCA-GCTGAAGGCATTGCGCGTAGTCCATGCCCGTAGAGGAAGTGT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCTGAGCCCACCGCAGGCTGAAGGCATTGCGCGTAGTCCCATGCCCGTAGAGGAAGTGT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAGGTCGCGGAGGAGCGTTGCCATTCAAGTGACTGCAGCAGCAGCGGCACCG-CTCGG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      953
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SQPEVYVAAPGESLEVRCLLKDAAVISWIKGGYILGPINRTVILIGEVIQIKGATPROS
CLYACTASRTYOSETIRVYVYWYDALISSGUEDENTGABEDYSCHUZUK
KHEKLLHAV PAANTYKEECPAGGNEMPTJARNLKNÖKEEKQEHLIGGYKVRNQHISLIN
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780 c 865 g 817 t
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180. 242
243. 2642
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/db_xref="GI:31374"
/db_xref="SWISS-PROT:P21802"
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/dev_stage="neonatal (1 day)"
180. .2645
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Pred. No. 0;
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1678	GCTGA	6	Дb
1772	GCTGACACTGGGCAAGCCCCTGGGAGAAGGTTGCTTTGGGCAAGTGGTCATGGCGC	1713	Qy
61	66	UT	рb
ب ر.	GGCAGGGGTCTCCGAGTATGAACTTCCAGAGGACCCAAAATGGGAGTTTCCAAGAGATAA	53	Q
6.5	3 CAACACCCCGCTGGTGAGGATAACAACACGCCTCTCTTTCAACGGCAGACACCCCCATGCT 1	1593	B 6
9	ACGTATCCCCCTGCGGAGACAGGTAACAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTC	43	ДЬ
59	ACGTATCCCCCTGCGGAGACAGGTAACAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTC	LΠ	Qy
1438		37	D.
5 37	GAAGAACACGAGCAAGAAGCCAGACTTCAGCAGCCAGCCGGTGTGTGT	7	5 8
-	TRACTGCATAGGGGTCTTCTTAATCGCCTGTATGGTGGTAACAGTCATCCTGTGCCGAAT	1413	, ç
	GCCAGCGCCTGGAAGAGAAAAGGAGATTACAGCTTCCCCAGACTACCTGGAGATAGCCAT	1259	В
1412	GCCAGCGCCTGGAAGAGAAAAGGAGATTACAGCTTCCCCAGACTACCTGGAGATAGCCAT	1353	Qy
25	TACGTGCTTGGCGGGTAATTCTATTGGGATATCCTTTCACTCTGCATGGTTGACAGTTCT	1199	Db
35	ACGTGCTTGGCGGGTAATTCTATTGGGATATCCTTTCACTCTGCATGGTTGACAGTTCT	9	Qy
9	GGACADAGAGTTGAGGTTCTCTATATTCGGAATGTAACTTTTGAGGACGCTGGGGAATA	13	Д
N	GACAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACTTTTGAGGACGCTGGGGAATA	23	δ
1232 1138	ATACGGGCCGGACGGCCTACCTCAAGGTTCTCAAGGCCGCCGGTGTTAACACCAC ATACGGGCCCGACGGACGTCCACGTCAAGGTTCTCAAGGCCGCCGGTGTTAACACCAC	07	D 1
	ATACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	17	Ş
7	TACACTGATGCCCAGCCCACACTCCAGTGCATCAAGCACGTGGAAAAGAACGACGGCAGTAA	101	B 5
1018	CGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGAGAGTTAGAGTTTGTC	95	유
1112	CGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGAGACGTAGAGTTTGTCTGG	105	Ş
Ū	9 CAATCACACGTACCACCTGGATGTTGTGGAGCGATCGCCTCACCGGGCCCATCCTCCAAGC	. 89	뫄
0	3 CANTCACACGTACCACCTGGATGTTGTGGAGCGATCGCCTCACCGGCCCATCCTCCAAGC	99	Į.
φ	9 TGTGGTCCCATCTGACAAGGGAAATTATACCTGTGTGGTGGAGAATGAAT	83	닭
9	3 TGTGGTCCCATCTGACAAGGGAAATTATACCTGTGTGGTGGAGAATGAAT	93	٥.
w	9 GGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTAIGGAAAG	77	ДD
	3 GGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTATGC	87	9
7	9 AGCCGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAGGAGTTTAAGCA	7.1	da
7	3 AGCCGGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAGGAGTTTAAGC	81	Qγ
718		65	문
- 4	3 AAAGATGGAAAAGCGGCTCCATGCTGTGCCTGCGGCCAACACTGTCAAGTTTCGCTC	75	δõ
	9 GGAAGATTTTGTCAGTGAGAACAGTAAC	59	Db
752	3 GGAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGGAGCACCATACTGGACCAACAC	7 69	γo

2493 GANTGANTGANTAGCCTCCCAAGAGACCTANCGANCTGTACATCAGAACCTCTGTAAACCGACCTTCTAAACCGACCTCCCAAGAGACCAAACGTCCAACGACCTCCCAAGAGACCAACGTCCCAAGAGACCAACGTCCGTACAACACTCCCCAAACATCAACCAAC	1679 AGTGGGANTGACAAAGACCATTGCCAAGGGGGTCACCGTGGACAGAGTGGACTTCAACT 1992 1833 AGATGATGCACAAAAAACCATTGCTTCTTCATCAGACCTTGAGAGATGGAGATGGACATTAAACT 1992 1879 AGATGATGCCACAGAAAAAACCTTTCTGATCTGGTGTCAGAGATGGAGATGGAGACT 1992 1879 AGATGATGCCACAGAAAAAACCTTTCTGATCTGGTGTCAGAGATGGAGATGGAGACT 1998 1893 CATTGGGAAACACAAAAAAAACCTTTCTGATCTTGGTGCTGCAACACACAAACAGCCTCCT 1952 1891 1111111111111111111111111111111111
HERCERRUM  DEFINITION  ACCESSION  ESSAGA D. G. 1.200062  KETWOODS  KETWOODS  SOURCE  ORGANISM  MARGINIA SELECTION  AUTHORS  STATUBE  TITLE  JOURNAL  MARGINIA SELECTION  EPERRUKE  JOURNAL  SOURCE  JOURNAL  SOURCE  JOURNAL  SOURCE  JOURNAL  SOURCE  FEATURES  FOR JEAN SUBMITTED  AUTHORS  STEIN BEET LO 3248)  AUTHORS  JOURNAL  SOURCE  JOURNAL  Genetics, Schiangenzahl 14, Glessen, Germany, 35392  JOURNAL  JOURNAL  Genetics, Schiangenzahl 14, Glessen, Germany, 35392  JOURNAL  JOURNAL  SOURCE  JOURNAL  SOURCE  JOURNAL  SOURCE  JOURNAL  J	Db 2759 GAGTANATNATTAGGAANAGTANTGAGCATATGAGCAGTTGAAACATTTATACAGTTGAAAACTTG 2818  OY 2913 TAATCTTCCCCAGGAGGAACAAAGGTTTCTGGAGCAGTTGGACGACCAGGCACCATG 2972

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                                      TACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGGGATCGCCTCACCGGCCC 1041
                       TACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGATCGCCTCACCGGCCC
                                                                    ATPATGGAAAGTGTGGTCCCATCTGACAAGGGAATTATACCTGTGTGGTGGAGAATGAA 981
                                                                                                                                                                  TYPICGETGCCCAGCGGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAG
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/product="fibroblast growth factor receptor 2"
/product="fibroblast growth factor receptor 2"
/note="A(885)-VG; Lys(292)-VGlu"
/phenotype="M. Crouzon"
/phenotype="M. Crouzon"
/ 737 c 808 g 788 t
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886
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/gene-"gft2"
/product-"fibroblast growth factor receptor 2"
/note-"exon U"
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Pred. No. 0;
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2181	TYGGCTTCCCAAAATGTATTCATCGAGATTTAGCAGCCGGAAATGTTTTGGTAACAGAA	2122	Qy
2121 1860	CAMPIGACCTTCANGGACTTOGTGTCATGCACCTACCACCTGGCCAGAGGCATGGACTGCACTGCATTTACTTTACTTTACTTTACTTTACTTTACTACTGCACCTACCAGCTAGGCAGGC	2062 1801	Db
2061 1800	CGAGCCCGGAGCCACCCGGGATGGAGTACTCCTATGACATTAACCGTGTTCCTGAGGAG 	7 0	DЬ
2001 1740	GATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAAGGCAACCTCCGAGAATAGCCTCGAGAATAGCCTGIIIIIIIIII	1681	Db Oy
1941 1680	ATRATIGANGATIGATIGGGANACACANGANTATCATAANTCTTCTTGGAGGCTTGCAGCACACAG ATRATIGANGATGATTGGGANACACANGANTATCATAANTCTTCTTGGAGGCTTGCACACAG ATGATGANGATGATTGGGANACACANGANTATCATAANTCTTCTTGGAGGCTTGCACACAG	1882 1621	Db Oy
1881 1620	AGARTETTGANACATGARGCCCACAGACANACGCCTTTCTCATGTGGTGTCAGAGATGGGGGGGGGG	1822	Db Qy
1821 1560	ATGGGGANGCAGTGGGAATTGACAAAGACAAGACCAAGGAGGGGGTZACCGTGGCCGTG 	5	Db
1761 1500	CCAAGAGATAAGCTGACAGTGGCAAGCCCCTGGGAGAAAGTTGCTTTGGGCAAGTGGCT 	44 6	. B &
1701 1440	CCCCCATGCTGGCAGGGGTCTC	38	) P 04
1641 1380	CATGAACTCCAACA	ω σ N	D CY
1581 1320	GCTGAC	1 20 5	oy Oy
1521 1260	GTGCCGAATGA          GTGCCGAATGA	20	Db Oy
1461 1200	GAGATAGCCATTACTGCATAGGGGTCTTCTTAATCGCCTGTATGGTGGTAACAGTCATC	14	Db Oy
1401 1140	TTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATTACAGCTTCCCCAGACTACCTG	1342 1081	Db Qy
1341 1080	GCTGGGGAATANAGTGCTTGGGGGGTAATTCTATTGGGATATCCTTTCACTCTGCATGG	1282	Db Qy
1281 1020	GTTAACACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACTTTTGAGGAC	96	dd dy
1221 960	AACGGCAGTAAATACGGGCCGGAGGGCTGCCCTACCTCAAGGTTCTCAAGGCCGCCGGT	1162 901	pb oy
1161 900	GTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAGTGGATCAAGCACGTGGAAAAG	1102 841	DЬ
840		781	D

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3261	ATGGATGTCCCAATGCACCTAGAAAATTGGTCTCTCTTTTTTTAATAGCTATTTGC	3202	Qy
2940	AAATTATGTATAAAATATATTATATATTTACAAGGAGTTATTTTTTGTATTGATTTT	2881	90
3201	AAATTATGTATAAATATATATATATTTACAAGGAGT	3142	οy
2880	GCACACACTTACAGAGCACAAATGCAGTATATAGGTGCTGGATGTATGT	2821	рь
3141	- 8	3082	9
2820	GTGGACGT6CGTTCT6CCTTCCTTGTTAATTTTGTAATAATTGGAGAAGATTTATG	2761	Db
3081	- 2	3022	οy
2760	ATGTAACCCCTCTCACCTGCCGTGCGTACTGGCTGTGGACCAGTAGGACTC	2701	Db
3021	AAGCCACCATGTAACCCCTCTCACCTGCCGTGCGTTCTGGCTGTGGACCAGTAGGACTCA	2962	9
2700	GTGGACTGCG	2641	Db
2961	CCCAGGAGGAGAAGAAGGTTTCTGGAGG	2902	Qy
2640	AGCATATGTGTAAAGATTTATAC	2581	Вb
2901	ATCAGAGGAGTAAATAATTGGAAAAGTAATCAG	2842	Qy
2580	CCTAGCTACACTGAGCAGGGAGACCATGCCTCCCAGAGCTTGTTGTCTCCACTTGTATAT	2521	망
2841	CTAGCTACACTGAGCAGGGAGACCATGCCCAGAGCTTGTTGTCTCCACTTGT	2782	Qy
2520	GGCAGTGTTAAAACATGAATGACTGTGTCTGCCTGTCCCCCAAACAGGACAGCACTGGGAA	2461	DЬ
2781	GCAGTGTTAAAACATGAATGACTGTGTGTGTGTGCCCGAAACAGGACAGGACAGTGGGAA	2722	9
2460	ACACATAAAC	2401	Вb
2721	TTTTTTCTCCAGAGCCCCATGCCTTACGAACCATGCCTTCCTCAGTATCCACACATAAAC	2662	Q
2400	-	2341	Db
2661	AACAGTATTCACCTAGTTACCCTGACACAAGAAGTTCTTGTTCTTCAGGAGATGATTCT	2602	Qy
2340	CGAATTCTCACTCTCACAACCAATGAGGAATACTTGGACCTCAGCCAACCTCTC	2281	Db
2601	TGGATCGAATTCTCACTCTCACAACCAATGAGGAATACTTGGACCTCAGCCAACCTCTC	2542	Ŷ
2280	AGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACGTTCAAGCAGTTGGTAGAAGAC	2221	Ф
2541	TTGGCATGCAGTGCCCTCCCAGAGACCAACGTTCAAGCAGTTGGTAGAAGAC	2482	γQ
2220	AGGAAGGACACAGAATGGATAAGCCAGCCAACTGCACCAACGAACTGTACATGATGATG	2161	В
2481	GAAGGACACAGAATGGATAAGCCAGCCAACTGCACCCAACGAACTGTACATGATGATG	2422	οy
16	TTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCCTGGAGGAACTTTTTAAGCTGCTG	10	B :
2421	ACTTTAGGGGGGCTCGCCCTACCCAGGGATTCCCCGTGGAGGAACTTTTTAAGCTGCTG	w	Ŷ
2100	GATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTCGGGGTGTTAATGTGGGAGATC	0	Db
2361	ATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTCGGGGTGTTAATGTGGGAGATC		Qy
0	TACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGGATGGCTCCAGAAGCCCTGTTT	9	B 5
2301	AAAAAAACACCACCAATGGGCGGCTTCCAGTCAAGTGGATGGCTCCAGAAGCCCCTGTTT	Ü	Ş
1980		92	g G
2241	AATGTGATGAAAATAGCAGACTTTGGACTCGCCAGAGATATCAACAATATAGACT	2182	γo
1920	TTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCCAGAAATGTTTTGGTAACAGAA 1	1861	В

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REFERENCE
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Best Local Similarity 99.9%;
Matches 3246; Conservative
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                           262 GGTACCGTAACCATGGTCAGCTGGGGTCGTTCATCTGCCTGGTCGTGGTCACCATGGCA 321
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Eukaryola, Metazoa, Chordata; Cranlata; Vertebrata; Eutaleostoml; Mammalia; Eutaleostom Primates; Ctarrfilni; Menindae; Homo. 1 (base; 10.0348) rimates; Ctarrfilni; Homindae; Homo. Steilberger D., Malliken, J. and Mueller, U. Reprimate the Menindae; Menind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H.sapiens fgfr2 gene.
Z69641
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FGFR2 gene: fibroblast growth factor receptor
Homo sapiens.
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Direct Submission
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                                                                                                                                                                                                                   /genc="fgfr2"
/note="T(880)->G; Trp(290)->Gly"
/phenotype="M. Crouzon"
/phenotype="M. 680 g 788 t
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880
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/dev_stage="infant"
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/isolate="proband 56"
/db_xref="taxon:9606"
/chromosome="10"
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/product≖"fibroblast growth factor receptor 2"
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1401	TRACAGETETECCAGGECTEGAAGACAAAGGACATTACAGETTCCCCAGACTACCTG	1342	D Qy
ο ω	CTGGGGAATATACCTGCTTGGCGGGTAATTCTATTGGGATATC 		B 3
1281 1020	TTAACACCACGGACAAAGAGATTGAGGTTCTCTAT2	96	B 8
1221 960	GGCAGTAAATAGGGCCGACGGGCTGCCCTAAGGTTCTCAAGGTCCCAAGGCCCCCCCGC 	90	, B 2
1161	TOTICIANGETTARAGTGATGCCCAGCCCCACATCCAGTGGATCAAGCACGTGGAAAAG	84	S & 5
1101	TOCTCCAAGCCGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGAGACTGAGAGACTTGAGAGTTTTTCCTCCACAGTGGTCGGAGAGACTGAGAGTTTTTCCTCCACAGTGGTCGGAGAGAGA	781	D
1041 780	AGGGTCGATCAATCAAACGTACACCTGGATGTTGTGGAGCGATGGCCTCACCGGCC 	72	8 8
981 720	TRATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTATACCTGTGTGGTGGAGAATGAA	661	D 04
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801 540	ACCAACACAGA,           ACCAACACAGA,	8 4	рь
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681 420	ACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCATCCGGAGAT	. 6	, B &
621 360	GCAGGCTAGAGACTCCGGCCTGTATGCTTGTACTGCAGTAGGACTV		B 6
561 300	GTGCACTTGGGGCCCAAC	0 4	p 04
501 240	TOGCTAGAGGTGGGCTGCCTGTTGAAAGATGCCGCCGTGATCAGTTGGACT	4 00	p
441 180	GAGCCACCAACCAAATACC	N ®	, p 54
381 120	A ACCTTGTCCCTGGCCCGGCCCTCCTTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAA  A ACCTTGTCCCTGGCCCGGCCCTCCTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAA  ACCTTGTCCCTGGCCCGCCCCTCCTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAA	6 2	Оу
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	ANGGANGGACAGAATGGATFAACCOAGCCAACTGCACGAACGTAACTGTACATGATCATG 	2422 2161	Оy
a= a	T-CACTTAGGGGGCTCGCCCTACCAGGGATTCCCGTGGAGGAACTTTTAAGCTGCT	2101	Db .5
7 7 7	ATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTCGG	04	₽ ₽
1 1 1	ACAAAAAAAACAACAATTAATTAATTAATTAATTAATTA	1981 2302	ov p
: 13	. 2	2242	Оу
3=2	ACAATGTGATGAAAATAGCAGACTTTGGACTCGCCAGAGATATCAACAATATAGACTAT	9	Db
ž	AATGTGATGAAAATAGCAGACTTTGGACTCGCCAGAGATATCTCAACAATATT	18	Q V
=ÿ	TIGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCAGAAATGTTTTGGTAACAG	2122	р <sub>О</sub> у
AC -	ATGACCTTCAAGGACTTGGTGTCATGCACCTACCAGCTGGCCAGAGGCATGGAGT	90	Вb
ž	CTTCAAGGACTTGGTGTCATGCACCTACCAGCTGGCCAGAGGCATGGAC	2062	Qy
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= 5	GATIGGCCTCTCTATGTCATAACTTGAGTATGCCTCTAAAGGGAACCTCCGAGAATAACC	1681	용 5
AG =	ATGATGAAGATGATTGGGAAACACAAGAATATCATJ	2 62	Db Db
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	AAGATGTTGAAAGATGATGACAAAGAAAAGATGTTTTTTTT	82	Q Q
- 6	TITLE TO THE TOTAL PROPERTY OF THE TOTAL PRO	50	Db 4
43.	CCAAGAGATAAGCTGACACTGGGCAAGCCCCCTGGGAGAAGGTTGCTTTGGGCAAGTC	1762	Q 6
- G	CCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAGAAGGTTGCTTTTGGGCAAGTG	70	Qy
111	ACCUCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCAGAGGACCCAAAATGGGA	1381	ф
3	CCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCAGAGGACCCAAAATGGGAG	64	Qy
8 - 9	1 TCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACACGCCTCTCTTCAACGGCAC	32	망
₹.	CCATGAACTCCAACACCCCGCTGGTGAGGATAACAACACGCCTCTCTTCAACGGCA	158	Qy
: :=:		126	Db
ä	AGCTGACCAAACGTATCCCCCCTGCGGAGACAGGTAACAGTTTCGGCTGAGTCCAGC	152	Qy
8=	TETTGCGGAATGAAGAACACGACCAAGAAGCCAGACTTCAGCAGCCAGC	120	Db
₽.	TGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTCAGCAGCCAGC	146	Qy
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2	AGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCCTGTATGGTGGTAACAGTC	140	Qy

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Crimates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3248)
1 (bases 1 to 3248)
Steinberger, D. and Mueller, U.
New point mutations in FGFR2 associated with Crouzon Syndrome
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Direct Submission
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/note="g(1037)->c; Cys342->Ser"
/phenotype="Crouzon Syndrome"
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13. 2478
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/chromosome="10q26"
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Ъ	121	GAGCCACCAACCAAATACCAAATCTCTCAACCAGAAGTGTACGTGGCTGCACCAGGGGAG 180	
Qy	442	TCGCTAGAGGTGCGCTGCTGTTGAAAGATGCCGCCGTGATCAGTTGGACTAAGGATGG	
DЪ	181	TCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCGCCGTGATCAGTTGGACTAAGGATGGG 2	
Ωу	502	TGCACTTGGGGCCCAACAATAGGACAGTGCTTATTGGGGAGTACTTGCAGATAAAGGGC 56	
Db	241		
Qγ	562	TCCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAGACAGTG	
Вb	301	CACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAG	
40	622	ATCTCATCCGGAGATGATGAGGATC	
Ф	361	TTGGTACTTCATGGTGAATGTCAC	
Qγ	682	CGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGAGCACCATACTGG 74	
Ъ	421	$\infty$	
Qγ	742	AAAAGCGGCTCCATGCTGTGCCTGCGGCCAACACTGTC	
Db	481	CCAACACAC	
Qy	0	CAGCCGGGGGGAACCCAATGCCATGCGGTGGCTGAAAAACGGG	
9	541	TCGCTGCCCAGCCGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAG 6	
δ	862	AGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTC 9	
Ъ	601	TTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTC 66	
δÃ	N	AAATTATACCTGTGTGGTGGAGAATG	
B	6	TTATGGAAAGTGTGGTCCCATCTGACAAG	
VΩ	982	GATCGCCTCACCGGCCC 1	
₽	721	ACGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGG	
Qy	4	GTAGAGTTT 1	
В	781	CCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGG	
Ϋ́	0	CCACATCCAGTGGATCAAGCACGTGGAAAA	
В	841	CTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAGTGGATCAAGCACGTGGAAAAAG 9	
νQ	6	TCAAGGCCGCCGGT 1	
g	ō	ACGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTCAAGGCCGCCC	
δ		GTTAACACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACTTTTGAGGAC 1281	
9	9	TTAACACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACTTTTGAGG	
Ϋ́	1282	CTATTGGGATATCCTTTCACTCTGCATG	
B	1021	CTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGGATATCCTTTCACTCTGCATGG	
¥	w	TG 1	
8	1081	TGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATTACAGCTTCCCCAGACTACCTG 11	
Ϋ́	402	TCTTCTTAATCGCCTGTATGGTGGTAACAGTCAT	
ŏ	141	AGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCCTGT	
Ϋ́	62	AGCCAGCCGGCTGTGCAC 152	
ĕ	1201	GTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTCAGC	

CCCCCAPTCTGGAAGGGTTCCGAATTGAAGACCCCTGGGAGAAGGCCCCGGGAGTATGAAGACCCCTGGGAGAAGGGTTCCGAGAGAGGATTGAAGAGAGGAGAGGCCCTGGGAGAAGGCCCCTGGGAGAAGGCCCCTGGGAGAAGGCCCTGGGAGAAGGCCCTGGGAAGAGAGAG
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keratinocyte growth factor
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Homo
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                                         keratinocyte growth factor receptor mRNA, complete cds
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Chan, A.M. and Aaronson, S.A.
Determination of ligand-binding specificity by splicing: two distinct growth factor receptors
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Mammālia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3106)
Miki, T., Bottaro, D.P., Fieming, T.P., Smith, C.L., Burgess, W.H.,
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// TEBRS 1 LOG = MYSMORP ICL/MVTHATILSLARP SES IL/DDITTLEP BEPPTKYO I
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FSPDPHPY EPPCLAVITHINGSWKT" 
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/protein_id="AAA36147.1"
/db_xref="G::186741"
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/cell_type="Epithelial cell"
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149 CCCAAGGACCACTCTTCTGCGTTTGGAGTTGCTCCCCGGCAACCCCGGGCTCGTCGCTTTC 61 TCCATCCCGACCCACGCGGGGCCCGGGGACAACACAGGTCGCGGAAGGAGCGTTGCCATTC CCCAAGGACCACTCTTCTGGGTTTGGAGTTGCTCCCCACAACCCCGGGGTCGTCGTCGCTTC 60 TATGGAAGAGAGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGC GATACCACATTAGAGCCAGAAGAGCCACCAACCAAATACCAAATCTCTCAACCAGAAGTG CTGGTCGTGGTCACCATGGCAACCTTGTCCCTGGCCCGGCCCTCCTTCAGTTTAGTTGAG TTGCGCGTAGTCCATGCCCGTAGAGGAAGTGTGCAGATGGGATTAACGTCCACATGGAGA AGTGACTGCAGCAGCAGC -GCAGCGCCTCGGTTCCTGAGCCCACCGCA -GCTGAAGGCA AAGTGACTGCAGCAGCAGCGGCAGCGCCTCGGTTCCTGAGCCCACCGCAGGCTGAAGGCA 180 TCCATCCCGACCCACGCGGGC-CGGGGACAACACAGGTCGCGGAGGAGCGTTGCCATTC CTGGTCGTGGTCACCATGGCAACCTTGTCCCTGGCCCGGCCCTCCTTCAGTTTAGTTGAG TATGGAAGAGGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGC Conservative 0; 62; Indels 18; Caps 325 120 208 360 445 300 385 240 267 420 505

1639	THATCGCCTGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACAAGAAG	1580	망
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1431	AGGAGATTACAGCTTCCCCAGACTACCTGGAGATACCATTACTGGATAGGGTCTTC  AAGGAGATTACAGCTTCCCCCAGACTACCTGGAGATAACCATTTACTGCATAGGGTCTTC  AAGGAGATTACAGCTTCCCCCAGACTACCTGGAGATAACCATTTACTGCATAGGGTCTTTC	1520	B 5
	AGGCCAACCAGTCTGCCTGGCTCACTGTCCTGCCAAAACAGCAAGCGCCTGGAAGAGAG	1460	8 8
1371	TATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAA	1321	γO
45	GCGGATGCTGGGGAATATATATGTAAGGTCTCCAATTATATAGGG	1401	В
ω 2	GAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGG	1261	οy
40		1346	Ъ
ر م	AGGTTCTCAAGGCCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTCTATATT	1201	οy
ω .	TGGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCGGACGGGCTGCCCTACCTC		Db
.20	GGATGAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTC	14	οy
28	GTCGGAGGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAG	Ν	Вb
4	TCGGAGGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAG	1081	VΩ
1225			Db .
2	AGCGATCGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGAATCCCAAATCCCTCCACACTC	0	οy
1165			DЪ
3	CCTGTGTGGGGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATCTTCTC	961	Ş
<u>س</u> و			В
5	GAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTAT	901	Q
0	CGGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTA	986	DЬ
0	GGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAA		οy
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925	GEOGGGG TO THE TOUR CHARLES AND THE BAAAAGCGGCTCCATGCTG		? ;
00	ARCARGRARGCACCATACTGGACCAACAGAAAAGATGGAAAAGCGGCTCCATGCTGTG	966	B 2
865	TCCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAG	, 0	) D
720	TCCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTTGTCAGTGAGAACAGTAAC	- 5	yo
805	AGTAGGA	746	В
660	AGTAGGACTGTAGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTC	601	УО
4	GAGTACTTGCAGATAAAGGGCCCCACACCTAGAGACTCCGGCCTCTATGCTTGTACTGCC	686	рь
0	GAGTACTTGCAGATAAAGGGCGCCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGC	541	Οy
œ		626	Оb
4	ATCAGTTGGACTAAGGATGGGGTGCACTTGGGGGCCCAACAATAGGACAGTGCTTATTGG	481	Q
เงิ	TACGTGGCTGCGCCAGGGGAGTCGCTAGAGGTGCGCTGCTTGAAAGATGCCGCCGTG		Дb
œ	TACGT6GCTGCGCCAGGGGAGTCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCGCCGT	421	Qy
565	5 GATACCACATTAGAGCCAGAAGAGCCACCAACCAAATACCAAATCTCTCAACCAGAAGTG	506	DЬ

12 AGACCAACGTTCAAGCAGTTGGTAGAAGACTTGGATGGAATTCTCACTACAACC	Oy 25
	Qy 24 Db 26
392 ATTECCGTGGAGGAACTTTTTAAGCTGCTGGAGGAACGAACAAGAATGGATAAGCCAGCC	ט ט
80 TGGTCCTTC	2 2
72 GTCA	. 2 2
12 CTCGCCAGAGATATCAACAATI	
52 TTAGCAGCCAGAAA	2 2
	N 1
032 TCCTATGACATTAACCGTGTTCCTGAGGAGCAGATG 1111111111111111111111111111111111	, N N
972 GCCTCTAAAGC	2 1
912 ATCATAAATCT            060 ATCATAAATCT	N L
852 GACCTTTCTGAT	2 1
79	0y 1 Db 1
732 CTGGGAGAAGGTTGCTTTGGGCAAGTGGTGATGGGGGAAGGGGGAATTGACAAGAC 	<b>_</b>
8 6	P P
7 6	• .
1552 CAGGTAACAGTTTCGGCTAAGTCAAGTCATCATCAACTCCAACACCGCGGTGGTAAGA 	Оу 1 рь 1
	Qy 1

1427	Db	OY 181 TIGGGGTAGTCCATGCCGTAGAGGAAGTGTGCAGATGGGATTAACGTCCACATGGAGA 240
1415 AAGGTTCTCAA	оу	0y         121 AAGTGAACTGCAGCAGCGGCAGCGCGAGGCTGAAGGCA           180         121 AAGTGACTGCAGCAGCAGCGCAGCGCTTCCTGAGCCCACGCAAGGCTAAAGGCA           180         111111111111111111111111111111111111
1355 TGGATCAAGCA	Db Qy	OY 61 TCCATCCCGACCCACGCGGGCCGCGGGACAACACAGGTCGCGAGGAGCGTTGCCATTC 120
1295 GTCGGAGGAGA 1141 TGGATCAAGCA	Qy Db	Oy 1 CCCAAGGACCACTCTTCTGCGTTTGGAGTTGCTCCCCACAACCCCGGCTCGTCGCTTTC 60
1235 GAGCGATCGCC	5 B 2	Query Match 62.6%; Score 2670.4; DB 6; Length 3244; Best Local Similarity 89.7%; Pred. No. 0; Matches 3029; Conservative 0; Mismatches 1; Indels 348; Gaps 1;
	ob oy	source 1344 /organisma"Homo sapiens" /organisma"Homo sapiens /ob_xref="taxon:9606"  BASE COUNT 861 a 795 c 852 g 736 t ORIGIN
901 CGAAACCAGCA            1115 CGAAACCAGCA	da Ao	JOURNAL Patent: WO 0194629-A 171 13-DEC-2001; Patent: WO 0194629-A 171 13-DEC-2001; AVAION PHARMSCOULTEATS (US) FEATURES LOCALIDA/Qualificies
841 CGGTGGCTGAA          1055 CGGTGGCTGAA	Qy VO	REFERENCE I. Augustus, M., Carter, K.C., Ebner, R., Endress, G., Auflinds Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Britan Horrigan, S., Soppet, D.R. and Meaver, M. Endress, G., TITLE Cancer gene determination and therapeutic screening using signature
781 CCTGCGGCCAA           995 CCTGCGGCCAA	Qq VQ	WS
721 AACAAGAGAGC	dg Vo	DEFINITION Sequence 17 from Patent WOU194029. ACCESSION AX339662.1 GI:18102640 KEYMORDS .
661 TCCGGAGATGA:	Qy	AX329662
601 AGTAGGACTGT/ 	Oy Db	Oy 2932 AAGAAGGTTTCTGGAGCAGTGGACTGC 2558
541 GAGTACTTGCAG            755 GAGTACTTGCAG	Qy	OY 2872 TAATCAGCATATGTGTAAAGATTTATACAGTTGAAAACTTGTAATCTTCCCCAGGAGAG 2931
481 ATCAGTTGGACT	Oy Db	Oy 2812 TCCCAGACCTTGTTGTCTCCCCTTGTATATATGGATCAGAGGAGTAAATAATTGGAAAAG 2871
421 TACGTGGCTGCC	Qy da	
361 GATACCACATTA	0y	Oy 2692 CCAMGCCTMCCTACATANCCACACMANACGGCAGTGTANAACHGAATGAATGACTGTGTCT 2751 Db 2840 CCATGCCTTCCTCAGTATCCACACATANACGGCAGTGTTANAACATGAATGACTGTGTCT 2899
	Qy	
241 TATGGAAGAGGA 	Qу	Oy 2572 GAGGAATACTTGGACCTCAGCCAACCTCTGGAAGAGTATTCACCTAGTTACCCTGGACACA 2631

1426		1427	Db
N	CGGAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGG	1261	Qy
N		4	Db -
1260	GGTTCTO	1201	O <sub>Y</sub>
4	TGGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTC		B &
20	TO STATE A TO A CETTO BAA A A A A A A A CETTO BAA TA A CETTO COCCO A COCCO	<u> </u>	2 5
1354	GTCGGAGGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCACATCCAG [	1295	, 5
29	AGCGATCGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAG	1235	DЬ
8	GAGCGATCGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTG	02	Qy
1234	GTGTGGTGGAGAATACGGGTCCATCAATCACCTACCACCTGGATGTTGT	1175	Db
1020	CCTGTGTGGTGGAGAATGAATACGGGTCCAT	6	Qy
1174	ACAAGGGAAATT	1115	Вb
960	GAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCC	901	γo
1114	CGGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTA	r.n	망
900	GGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGT	841	γQ
1054	CCGGGGGGAACCCAATGCCAACCAT	995	рb
840	CTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGGAACCCAATGCCAACCATG	781	Qy
994	TCCATGCTGTG	35	Dъ
780	AAGAGAGCACCATACTGGACCAACACAGAAAAGATGGAAAAGCGGCTCCATGCTGTG	-	Qy
934	AGTGAGAACAGTAAC	875	Db
720	CCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAAC	661	Qy
874	AAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCA	815	Db
660	TAGGACTGTAGACAGTGAAACTTGGGTACTTCATGGTGAATGTCACAGATGCCCATCTCA	601	φ
814	CTCTATGCTTGTACTGCC	755	рb
600	AGTACTTGCAGATAAAGGGGGCCCAGGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCC	541	Qy
754	ດ-	695	Db
540	TCAGTTGGACTAAGGATGGGGTGCACTTGGGGGCCCAACAATAGGACAGTGCTTATTGGG	481	Qy
694	CTGTTGAAAGATGCCGCCGTG	35	Db
480	ACGTGGCTGCCCCAGGGGAGTCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCGCCGTG	μ	Qy
634	AGAAGTG	575	DЬ
420	ATACCACATTAGAGCCAGAAGAGCCACCAACCAAATACCAAATCTCTCAA	361	9
574		15	В
360	TGGTCGTGGTCACCATGGCAACCTTGTCCCTGGCCCGGCCCTCCTTCAGTTTAGTTG	21	οy
514	TATGGAAGAGGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGC 5	455	Db
300	ATGGAAGAGGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTG	241	Qy

2460	401 GAGGAACTTTTTAAGCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCC	
Ñ	207 GGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCCAGGGATTCCCCTG	Db 2
2400	341 GGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGGCTCGCCCTACCCAGGGATTCCCGTG	
2340 2206	201 AUSCULCKARAGICCICTTTGATRAGGTATRACACTCATCAGAGTAGATCGGTCCTTC	B 4
2146	087 GATATCAACAATATAGACTATTACAAAAAAAACCCCAATGGGCGGCTTCCAGTCAAGTGG	
2280	221 GATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGG	·
2086	027 AGAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGACTTTGGACTCGCCAGA	-
J (	161 AGAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGACTTTTGGACTCGCCACA	Qy 2
2026	967 CTGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCC	•
, ,	101 CTGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCATCAGATTTAACCA	0y 2
2100	041 ATTAACGGTGTTCCTGAAGAACAAGTGACCTTCAAGGACTTGGTGTCATGCACCTACCAG	Db 1
1906	847 GGCAACCTCCGAGAATACCTCCGAGCCCGGAGGCCACCCGGGATGGAGTACTCCTATGAC	_
2040	981 GGCAACCTCCGAGAATACCTCCGAGCCCGGGAGGCCACCCGGGATGGAGTACTCCTATGAC	0у 1
84	787 CTTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAA	Db 1
· •	921 CTTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAA	
78	727 GATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGAAACACAGAGAATATCATAAAT	Db 1
92	.861 GATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGAAACACAAGAATATCATAAAT	
72	1667 GAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACCTTTCT	-
œ .	801 GAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGATGCCACAGAGAAGACCTT	
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80	41 GGTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGGAATTGACAAAGACAAGCCC	
60	1547 GAGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAGAA	
7.4	GACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAG	
1680 1546	1487 CGCCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCA	B 5
1486	427 GTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACACAC	
1620	561 GTTTCGGCTGAGTCCAGCTCCTCCATGA	
1426	27	
1560	CAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAA	
1426	1427	
1500	1 TG	
1426	1427	
4	AGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCG	
42		Db
1380	1321 ATATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATT	Qy

### RESULT 11 HUMKSAMIII LOCUS DEFINITION

HUMKSANIII

3244 bp mRNA linear PRI 06-JAN-1995
HUMAG Secreted fibroblast growth factor receptor (K-sam-III) mRNA,
complete cds.

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KEYWORDS
SOURCE
ORGANISM
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Matches 3029; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGGAAGAGGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGC
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CTGGTCGTGGTCACCATGGCAACCTTGTCCCTGGCCCGGCCCTCCTTCAGTTTAGTTGAG
                                                                                                                    TATGGAAGAGGACCGGGGATTGGTACCCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGC
                                                                                                                                                                                                                                         TTGCGCGTAGTCCATGCCCGTAGAGGAAGTCTGCAGATGGGATTAACGTCCACATGGAGA
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M87771.1 GI:186781
Keam-III. Élbroblast growth factor receptor.
Homo sapiens cunA to mRNA.
Homo sapiens
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Proc. Natl. Acad. Sci. U.S.A. 89 (7), 2960-2964 (1992)
92212948
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Sugimura, T. and Terada, K.
K. sam gene, encodes secreted as well as transmembrane receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutoleostomi,
Mammalia, Butherla, Primates, Catarrhini, Hominidae, Homo.
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ASKGHLREYLAARRPGEKEYSUDIRBYPEROMTEKOLVSCTYQLARGHETHASKOCHH
RDLAARRVLYVERUNWKH ADGLARGINHLOY KKTTWAGLZUWKMAPEALEDBYTH
GSDWASFQYLMHEIFTLGGSPYFGIPVEELFKLLKGGHRHOKFANCTREITMOHRDOW
HAVPSORDTFKOLVEELDRILITTTMEEYLDLSOPLEQYSFSYDDTRSSCSSGODGVF
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488. .2605
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/codon_start=1
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AGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCC 144	≨	Ĺ	Qy
1426	27	14	Дb
TATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATT 1380	21 ATA	13	δō
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GAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATT	61 CGG	12	γQ
AAGGTTCTCAAG1426	15 AAG	14	밁
CAAGGCCGCCGGTGTTAACACCACGGA	01 AAG	12	Qγ
GATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGCCTGCCCTACCT	8	13	ф
GATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTAC	41 TGG	11	οy
CGGAGGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCC	95 GTC	12	рь
CGGAGGAGACGTAGAGTTTGTCTG	- 7	10	Qy
CGATCGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAC	35 GAG	12	망
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CTGTGTGGTGGAGAATGAATACGGGTCCATCAATCACGTACCACCTGGATGTTGT	75 ACC	11.	몽
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PAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTAT 1174	5 CG7	111	рb
AAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATT		9	Qγ
GGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGGAGCATCGCATTGGAGGCTACAAGGTA 1114	G	105	В
GCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAG	1	84	QΥ
TGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGAACCCAATGCCAACCATG 1054	95 CCTGC	99	Вb
GCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGAACCCAATGCCAACCAT	_	78	Qγ
AACAAGAGAGCACCATACTGGACCAAGACACAGAAAAGATGGAAAAGCGGCTCCATGCTGTG 994	ū	. 93	В
NGAGCACCATACTGGACCAACACAC	-	72	δ
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CGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTTGTCAGTGAGAAA	1 700	55	δô
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2580	TTCAAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCTCACAACCAATGAGGAATAC 2	2521	Qγ
38	CGAACTGTACATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACG	327	Db
ū	CGAACTGTACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACG	2461	Qy
2460 2326	CAGGAACTTTTTAAGCTGCTGAAGGAAGGAACACAAATGGATAAGCCAGCC	2267	₽ 5
26	GGGTTANTGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCCTG	207	D D
0	GGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCGTG	2341	οy
2340	THE CONTROL OF THE	147	뮹 .
	TGGCTCCAGAAGCCCTTCTTTTGATAGAGACACACACACA	281	o O
28	VALARI CAMUMATA RIAGACITATTIACAAAAAGACCACCAATIGGGCGGCGCTTCCAGGTCAAGTGG 	087	문 4
2086	GAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGACTTTGGACTCGCCAGA	027	2 8
2220	AGAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGACTTTGGACTCGCCAGA	61	νo
2026	CAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCC	967	В
2160	CCAAAAATGTATTCATCGAGATTTAGCAGCC	Ē	Qy
1966	CGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAG	907	οb
10	CCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAG	2041	Qy
	GCAACCTCCGAGAATACCTCCGAGCCCGGAGGCCACCCGGGATGGAGTACTCCTATGAC	1847	рь
04	AACCTCCGAGAATACCTCCGAGCCCGGGAGGCCACCCGGGATGGAGTACTCCTATGAC	981	Qy
84.	CTTCTTGGAGCCTGCACACAGGATGGGCCTCTATGTCATAGTTGAGTATGCCTCTAAAA	1787	рь
98	TGCACACAGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAA	921	Qy
78	GATCTGGTGTCAGAGATGAGATGATGAAGATGATTGGGAAACACAAGAATATCATAAAT	1727	망
92	ATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGAAACACAAGAATATCATAAAT	1861	Qγ
72	GAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAAGACCTTTCT	1667	D <sub>b</sub>
σ	AGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACCT	1801	Qy
1800	GSTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATGACAAAGACAAGCCCAAG	1607	B 5
1606	AGGACCCAAAATGGGAGTTTC	1 5	, B
1740	SGCAAGCCCCTGG	00	οy
1546	CGCCTCTCTTCAACGGCAGACACCCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCA	1487	DP
1680	CCTCTCTTCAACGGCAGACACCCCCCATGCTGGCAGGGGGTCTCCGAGTATGAACTTCC	m	Qy
4	CAGCTCCT	1427	Db
62	TTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAAC	Ċ	Qy
1426		1427	Db
o,	CAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAG	1501	Qy
1426		1427	Db
1500	TGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTC	1441	Qy

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KEYWORDS SOURCE ORGANISM RESULT 12 AF211257 REFERENCE VERSION ACCESSION DEFINITION complete cds. AF211257 AF211257.1 G1 Canis familiaris Canis familiaris BukaryOta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butherla; Carnivora; Fissipedia; Canidae; 1 (bases I to 3809) AF211257
3809 bp mRNA linear MAM 05-JAN-200 Canis familiaris fibroblast growth factor receptor 2 (FGFR2) mRNA, GI:6671356 Euteleostomi; Canis. MAM 05-JAN-2000

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Best Local Similarity

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Nguyen,T.L. and Chev.
Direct Submission
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Keratinocyte Growth Factor Receptor in Canine Prostatic Epithelial
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/note="keratinocyte growth factor receptor"
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/cell_type="epithelium"
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GCTTCCAGTCAAGT 2278	9 GAGATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGG	2219	Qy
CTTTGGACTGGCC	AATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGA	69	망
CTTTGGACTCGC	CAGAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGA	2159	δ
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GTOGTGTACCTACC 163		57	Db
GTCATGCACCTAC	ACATTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGT	0	Qy
GGAGTATTCCTATG 2030 GGAGTATTCCTATG 1572	AGGCAACCTCCGAGAATACCTCCGAGCCCGGAGGCCACCCGGAG 	1979	P 64
GAGTATGCCTCGA 151	ATCTCCTTGGAGCCTGTACTCAGGATGGCCCACTCTACGTCATTGT	4.	В
TGAGTATGCCTCTA 1978	ATCTTCTTGGAGCCTGCACACAGGATGGGCC	1919	Q
AAAAATATCAT	CTGATCTAGTGTCAGAGATGAGATGAAGATGAATGGAAAACA	1393	Db
CAAGAATATCATAA 1918	CTGATCTGGTGTCAGAGATGGAGATGATGAAG	1859	Q.
AGAGAAAGATCTTT 1392		1333	DЬ
AGAAAGACCTT	AGGAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCAC	1799	γo
CAAAGAGAAGCCCA 1332		N	D b
AAAGACAAGCCC	AAGGTTGCTTTGGGCAAGTGGTÇATGGCGGAAGCAGTGGGAATTGAC	1739	γo
AAACCTCTGGGG			₽
AAGCCCCTGG	CAGAGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGC	1679	Ωy
GAGTATGAACTG	CGCGCCTCTCCTCAACAGCAGACACCCCCATGCTGGCAGGGGTCTCC	ш.	Db
GAGTATGAAC	CACGCCTCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCC	1619	οy
GTGAGGATAAC	CAGTGTCTGCTGAGTCCAGCTCCTCTATGAACTCCAACACTCCGCTG	1093	Вb
GTGAGGATA	CAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTG	1559	γQ
GCGGAGACAGGTAA 1558                 GCGGAGACAGGTAA 1092	TCAGCAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTG	1499 1033	P 04
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CAAGAAGCCAGACT 1498	TATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACC	1439	Qy
GTCTTCCTAATT	ACGGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGG	913	D
GTCTTC	TACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGG	1379	40
AGAAAAGGAG	CTGCCTGGCTCACTGTCCTGCCAAAACAGCAAGCTCCTGT	853	망
SAAGAGAAAAGGAGA 1378	CATGGTTGACAGTTCTGCCAGCGCCTGG	1328	Qy
TATAGGGCAGGCCA 852		793	DЪ
ATTGGGATATC	AACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCT	1268	Qy
TTCAATG 792	CAMBOLOUCUS ISTANCECCAUDOCARDONAL STOSTANCE   CAMBOLOUCUS ISTANCECCAUDOCADA   CAMBOLOUCUS ISTANCECAUDOCADA   CAMBOLOUCUS ISTANCECAUDOCACAUDOCADA	739	g ç
TACCTCAAGGTT	ACACGTAGAAAAGAACGGGAGCAAATACGGGCCCGATGGGTTGCCG	7	g D
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347 2888	393 ACCGACCAGACTGCAAAAATACTTTGCCTTTCAGGGAAAATGGGTAAACGTTAA 3	Db Qy
3292 3828	69 TCTTTT	B 6
3235 2768	176 GGAGTTATTTTTGTATTGATTTAAATGGATGTCCC.   1	D 09
3175 2708	117 GTGCT	. B 64
3116 2648	US7 GTAATAATTGGAGAAGATTTATGTGCAGGACACATGAGAGCACAAATGGAGTATETA 	B 64
3056 2588	999 CTGGCTGTGGACCAGTMGGACTCAAGGTGGACTGC-GCCTTCCTGCTAATTTT	b da
2997 2528	348 GTTTCTGGAGCAGTGGACTGCCACAAGCCACCATGTAACCCCTCTCACCTGCCAGGGCTAGCAGTGCAGGGCTAGAGCAGGGCAGGGCATGAACCCCTCTCACCTGCAGGGCAGGAGAGAGA	p dy
2937 <b>247</b> 1	879 CATATGTGTADAG-ATTTATACAGTTGAAAACTTGTAATCTTCCCCAGGAGGAGAAGAAG	Db Qy
2878 2411	819 GCTTGTTGTCCCACTTGTATATGGATCAGGAGTAAATAATTGGAAGAGTAATCAG 	p dg
2818 2351	759 CCCAACACGACAGGCACTGGGAACCTAGCTACACTGAGCAGGGAGACCATGCCTCCCAGA	D 04
2758 2292	1699 TICCTEAGTATECAGACATAAACGGCAGTGTTAAAACATGAATGACTGTGTTGCCCTGTG 	D Qy
2698 2232	549 CTTGTTCTTCAGGAGATGATTCTGTTTTTTCTCCAGACCCCATGCCTTACGAACCATGCC 11111111111111111111111111111111111	B 6
2638 2172	579 AGTTGGACCTCAGCAACCTCTCGAACAGTATTCACCTAGTTACCCTGACACAGAGGT 	рь
2578 2112	519 053	D Qy
2518 2052	459 CCAACGAACTGTACATGATGATGAGGGACTGTTGGCATGCAGTGCA 	. B 54
2458 1992	399 TGGAGGAACTTTT	DB Qy
2398 1932	ض ن	D 04
2338 1872	00 N	B 5
1812	753 GAGATATCAACAATATAGACTATTACAAAAAGACCACAAN	25

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HUMFGFR2A
LOCUS
DEFINITION HUMPGFRA 3080 bp mRNA linear PRI 08-NOV-1994 HOMO Sapiens fibroblast growth factor receptor 2 IIIb (FGFR2) mRNA, complete cds. M97193 GI:182566

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J. Biol. Chem. 267 (29),
93016048
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Dell,K.R. and Williams,L.T.

A novel form of fibroblast growth factor r
splicing of the third immunoglobulin-like
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/protein_id="AAA52449.1"
/db_xref="GI:182567"
/db_xref="GDB:G00-127-273"
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/db_xref="taxon:9606"
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                                                                                                           CGGAATGTAACTTTTTGAGGACGCTGGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGG 1320
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   CAGGCCAACCAGTCTGCCTGGCTCACTGTCCTGCCAAAACAGCAAGCGCCTGGAAGAGAA
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                                                                                                                                           AAGGTTCTCAAGCACTCGGGGATAAATAGTTCCAATGCAGAAGTGCTGGCTCTGT-----
                                                                                              -TCAATGTGACCGAGGCGGATGCTGGGGAATATATATGTAAGGTCTCCAATTATATAGGG
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AGTAGGACTGTAGACAGTGAAACTTGGTACTTCATTGGTAATGTCACAGATGCCATCTCA
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	2451 2792	2 ATTCCCGTGGAGGAACTTTTTAAGCTGCTGAAGGAAGGACAGAGAATGGATAAGCCAGCC	239 273
	2391 2732	TGGTCCTTCGGGTTGTTAATGTGGGAGATCTTCACTTTAAGGGGGTCGCCCTACCCAGGG 	on w
	2331 2672	72 GTCAAGTGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGATGTC	227 261
	2271 2612	2 CTGCCCGGAGATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTTCGA	255
	2211 2552	52 TTAGCAGCAGAAATGTTTTGGTAACAGAAAAGAATGTGATGAAAATAGCAGACTTTGGA 52 TTAGCAGCCAGAAATGTTTTGGTAACAGAAAAGAATGTGATAAAATAGCAGACTTTTGGA 93 TTAGCAGCAGAAATGTTTTGGTAACAGAAAACAATGTGATAAAATAGCAGACTTTTGGA	24
	2151 2492	92 ACCTACCAGCTGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGAT	24
	2091 2432	2 TCCTATGACATTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGC 2 TCCTATGACATTAACCGTGTTCCTGAGGAGCAGTGACCTTCAAGGACTTTGGTGTTCATGC 73 TCCTATGACATTAACCGTGTTCCTGAGGACCAGATGACCTTCAAGGACTTTGGTGTTCTATGATCATCATTGGTGTTTGGTGTCATGAC	20
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	1971 2312	ATCATAANTCYTCTTGGAGCCTGCACAGAGGGCCTGCTATGTCATAGTTGAGTÀT 	22
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	1851 2192	92 ANGCCCMAGAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAA 33 ANGCCCMAGAGAGGGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAA 34 ANGCCCMAGAGAGGCGTCACCGTGGCCGTGAAGATGTTGAAAGATGTGCACAGAGAAAA	7 17 5 21
	1791 2132	32 CTGGGAGAAGGTTCCTTTGGCCAGTGGTCATGGCGGAACCAGTGGGAATTGACAAAGAC 	y 17
	1731 2072	772 GAACTYCCAGAGGACCCAAANTGGGACTYTCCAAGAGATAAGCTGAGACTGGGCAAGCCC 	y 16
	1671 2012	112 ATACAMCACCCTTCTTCAACGGCAGGCACCCCATGCTGGCAGGGGTCTCCCAGTAT 153 ATAACAACACGCTTCTTCAACGGCAGACACCCCATGCTGCCAGGGGTCTCCCGAGTAT 154 ATAACAACACGCTCTTCTTCAACGGCAGACACCCCXTGCTGCCAGCGGGGTCTCTGAACGGCTGTTCTAACGGCAGACACCCCXTGCTGCCAGCGGCGGCAGACACCCCCATGCTGCAGCAGCAGCCAGC	y 16 b 19
. –	1611	552 CAGGTAACAGTTTGGGCTGAGTGCAGCTCCTCGATGAACTTCGAACACCGCGGTGGTGAGG 393 CAGGTAACAGTTTGGGCTGAGTGCAGCTCCTCGATGAACTTCCAACACCCCGTTGTTATGT 194 CAGGTAACAGTTTGGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCCTTGGTATGT	у 15 b 18
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                        ATGGTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGGATGACACCGATGGTGCG
                                       ATGGTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGAGGATGACACCGATGGTGCC 693
                                                                        GACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAGACAGTGAAACTTGGTACTTC
                                                                                      GACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAGACAGTGAAACTTGGTACTTC
                                                                                                                        CCCAACAATAGGACAGTGCTTATTGGGGAGTACTTGCAGATAAAGGGCGCCCACGCCTAGA
                                                                                                                                      CCCAACAATAGGACAGTGCTTATTGGGGAGTACTTGCAGATAAAGGGCGCCACGCCTAGA
                                                                                                                                                                                                                           AAATACCAAATCTCTCAACCAGAAGTGTACGTGGCTGCGCCAGGGGAGTCGCTAGAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATGCCTTCCTCAGTATCCACACATAAACGGCAGTGTTAAAACATGA 2739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAGTTCTTGTTCTTCAGAAGATGATCTGTTTTTTCTCCAGACCCATGCCTTACGA 2691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P. Method for inhibiting the expression of a target gene Patent: WO 10255693-A 85 18-JUL-2002; Ribopharma AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
AX481471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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ilarity 100.0%;
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/db_xref="taxon:9606"
604 c 656 g 53
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85 from Patent W002055693.
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1833	74 GTGGGAATTGACAAAGACAAGCCCCAAGGAGCGGTGACCGTTGCCCGTGAAGATGTTGAAA	, 17	õ
1500	4 CTGACACTGGGCAAGCCCCTGGGAAAAGCTTTTTGGGCAAGTGGTCATGACAA 	17	D QQ
71	AGGGGTCTCCGAGTATGAACTTCCAGAGGACCCAAANTGGGAGTTTCCAAGAGATAA 	16	pr 8
1653 1380	4 AACACCCCGCTGGTGAGGATAACAACACGCCTCTCTTCAACGGCAGA 	y 159 o 132	Db Oy
	CGTATCCCCCTCCCGGAGACAGGTAACAGTTTCGGCTGAGTTCCACCTCCTCCATCAACTCC   CGTATCCCCCTGCCGGAGACAGGTAACAGTTTCGGCTGAACTCCACCTCCTCCATCAACTCC   CGTATCCCCCTGCCGGAGACAGGTAACAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTCC   CGTATCCCCCTGCCGAGAACAGGTAACAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTCC	y 153 b 126	B 8
1533 1260	4 AGANCACGACCAAGAACCAGACTTCACCAGCCACCACCACCACCACAACTTACCACAACTTACCACAACTTACCACAACTTACCACAACTTACCACAACTTACCACAACTTACCACAACTTACCACAACA	7 147 5 120	Dr 99
1473 1200	4 TACTGCATAGGGTCTTCTTAATCGCCTGTATGGTGCTAACAGTCATCCTGTGCCGCAATG 	, 141 5 114	P 94
1413 1140	CARGUECTEGARGACAAAGGRATTSCACCTTCCCARCTACCTGGAGATAGCCATT 	, 135 5 108	D
1353 1080	A ACGICTIGACAGGIAATICTATIGAGATANCCTTICACTCTCANGGITAAAGGITIAA ACGICTIGACAGGIAATICTATIGAGATANCCTTICACTCTGCANGGITIAACAGTTCTG 11. ACGICTIGACAGGIAATICTATIGAGATANCCTTTCACTCTGCANGGITIGACAGTTCTG	129	B 8
1293 1020	GACANAGAGATTGAGGTGTGTGTATATTGGGAATGTAAGTTTTGAGGACGGTGGGGAATAT 	, 123	56 76
1233 960	- TACGGCCCGAGGGCTGCCCTACCTCAAGGTTCTCAAGGCCCCGGTGTTACACCCCAC   TACGGCCCGACGGCCTGCCCTACCTCAAGGTTCTCAAGGCCGCGGTGTTAACACACAC	90	B 3
1173 900	TACAGTGATGCCCACCCCACTCCAGTGGATCAAGCACCTGGAAAACAACGGCACTGAAAACAACGCCACTGAAACAACGCCACTGAACAACGACCTGGAAACAACGACGCACTGAACAACGACGCACTAAACAACGACGACGAGAAACAACGACGACGAGAAACAACGACG	111	80 94
1113	GANTTOCCGCCAAATGCCTCCACACTGGTCGGAGGAGACCTAGAGTTTGTCTCCACACTTGTCTCTCCACACTGGTCGGAGGAGACCTAGAGTTTGTCTGCCACACTGTCGTCGGAGGAGACGTAGAGTTTGTCTGCAAGGTT	105	B 6
1053	4 ANTCACACGTACCACCTGGATGTTGTGGAGCGATCGCCTCACCGGCCCATCCTCCAAGCC	99	P Q
993 720	4 GEGGECCATCTGACAAGGAAATAAACCTGTGTGGGAGAATAAATA	93	Ор
933	A GAGANTGCANTGCAGCTPCAAGGTACGAACCAGCGCGCGGGGCGTCATTATGCAAAGT   A GAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTATGGAAAGT   A GAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTATGGAAAGT	8 <b>7</b>	DP OA
873 600	4 CCCGGGGGGAACCCAATGCCAACCATGGGGTGGCTGAAAAACGGGAAGGAGTTTAAGCAG 	81 54	DP GA
813 540	A ANGATGGAAAAGCGGCTCCATGCTGTGCCTGCGGCCAACACTGTCAAGTTTCGCTGCCCA	75 48	DP 64
480		42	рb

	LACATGA 2466 .	246	Dъ	
	ACATGA 27	7	γo	
2460	L GACCCCATGCCTTACGAACCATGCCTTCCTCAGTATCCACACATAAACGGCAGTGTTAAA	240:	Дb	
2733	GACCCCATGCCTTACGAACCATGCCTTCCTCAGTATCCACACATAAACGGCAGTGTTAAA	2674	Qy	_
2400	CCTAGTTACCCTGACACAAGAAGTTCTTGTTCTTCAGGAGATGATTCTGTTTTTTCTCC	2341	дь	
2673	- ^	2614	Оу	
2340	CTCACTCTCACAACCAATGAGGAATACTTGGACCTCAGCCAACCTCTCGAACAGTATTC	2281	Db	
2613	CTCACTCTCACAACCAATGAGGAATACTTGGACCTCAGCCAACCTCTCGAACAGTATTCA	2554	Qy	
2280	CATGCAGTGCCCTCCCAGAGACCTACGTTCAAGCAGTTGGTAGAAGACTTGGAT	2221	DЬ	
2553	CATGCAGTGCCCTCCCAGAGACCAACGTTCAAGCAGTTGGTAGAAGACTTGGATCGAATT	2494	Qy	
2220	AGAATGGATAAGCCAGCCAACTGCACCAACGAACTGTACATGATGAGGGACTGTTGG	2161	DЪ	
2493	AATGGAT	2434	Оу	
2160	GGCTCGCCCTACCCAGGGATTCCCGTGGAGGAACTTTTTAAGCTGCTGAAGGAAG	2101	Db	
2433	GGCTCGCCCTACCCAGGGATTCCCGTGGAGGAACTTTTTTAAGCTGCTGAAGGAAG	2374	Qy	
2100	ACTCATCAGAGTGATGTCTGGTCCTTCGGGGTGTTAATGTGGGAGATCTTCACTTTAGGG	2041	Db	
2373	ACTCATCAGAGTGATGTCTGGGTCCTTCGGGGTGTTAATGTGGGAGATCTTCACTTTAGGG	2314	Qy	
2040	ACCAATGGCGGCTTCCAGTCAAGTGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATAC	1981	Дb	
2313	ACCAATGGGCGGCTTCCAGTCAAGTGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATAC	2254	Qγ	
1980	AAAAGACC	1921	ф	
2253	AAAATAGCAGACTTTGGACTCGCCAGAGATATCAACAATATAGACTATTACAAAAAAGACC	2194	Оy	
1920	AAATGTATTCATCGAGATTTAGCAGCCAGAAATGTTTTGGTAACAGAAAAACAATGTGATG	1861	Db	
2193	AGATTTAGCAGCCAGAAATGTTTTGGTAACAGAAAACAATGTGATG	2134	γQ	
1860	AAGGACTTGGTGTCATGCACCTACCAGCTGGCCAGAGGCATGGAGTACTTGGCTTCCCAA	1801	망	
2133		2074	Qy	
1800	CCACCCGGGATGACTACTCCTATGACATTAACCGTGTTCCTGAGGAGCAGATGACCTTC	1741	Db	
2073	CACCCGGGATGGAGTACTCCTATGACATTAACCGTGTTCCTGAGGAGCAGATGACCTTC	2014	Qγ	
1740	AGCCCGGAGG	1681	Db	
2013	TATGTCATAGTTGAGTATGCCTCTAAAGGCAACCTCCGAGAATACCTCCGAGCCCGGAGG	1954	Qy	
1680	AGGATGGGCCTCTC	1621	Db	
1953	GGGAAACACAAGAATATCATAAATCTTCTTGGAGCCTGCACACAGGATGGGCCTCTC	1894	Qy	
1620	ATG	1561	Дb	
1893	GATGATGCCACAGAGAAAGACCTTTCTGATCTGGTGTCAGAGATGGAGATGAAGATG	1834	Qy	
1560	GTGGGAATTGACAAAGACAAGCCCAAGGAGGCGGTCACCGTGGCCGTGAAGATGTTGAAA	1501	DЬ	

RESULT 15
HUMTK14
LOCUS
DEFINITION
HUMAN fibroblast growth factor receptor mRNA, complete cds.
ACCESSION M55614 M37715
VERSION M55614.1 GI:339710

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Best Local
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Matches 2472; Conserv
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MEDLINE
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562 GCCACGCCTAGAGACTCCGGCCTCTATGCTTCTACTCCAGTAGAGACTGTAGACAGTGAA 621
301 GCCACGCCTAGAGACTCCGGCCTCTATGCTTCTACTCCCAGTAGACTGAGACTGTAGACAGTGAA 360
                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 GGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGCCTGGTCGTGGTCACCATGGCA 321
                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGCACTTGGGGCCCAACAATAGGACAGTGCTTATTGGGGAGTACTTGCAGATAAAGGGC 561
                                                                                    GTGCACTTGGGGCCCCAACAATAGGACAGTGCTTATTGGGGAGTACTTGCAGATAAAGGGC
                                                                                                                                                                                             TCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCGCCCTGATCAGTTGGACTAAGGATGGG 501
                                                                                                                                                                                                                                                         GAGCCACCAAACCAAATCTCTCAACCAGAAGTGTACGTGGCTGCGCCAGGGGAG
                                                                                                                                                                                                                                                                                                                                             TCGCTAGAGGTGCGCTGCTTGAAAGATGCCGCCGTGATCAGTTGGACTAAGGATGGG
                                                                                                                                                                                                                                                                                                                                                                                     ACCTTGTCCCTGGCCCGGCCCTCCTTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Manmalla: Eutheria: Primates: Catarrhini; Hominidae: Homo: 1 (bases: 1 to 248); Parasistante: Parasistante: Blanquet.P.R.. Champlon-Arnaud,P., Gesnel,M.C., Terrigila,A., Courtois,Y. and Breathnach,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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KMEKRLHAVPAANTVER RCPAGGIPHTWHINLIKHGKER (OBHRIGGYVRNO)HSLIH
ESVVESDKONTYCVNENEYGS INFTYHLDVYESSPERRE ILOACLE ANASTYVGGNYE
VCKYYSDKOPHIONI ENTEKNESKYCEPGLIPELIK LIKKEKESTRASETYLTIKE
VCKYYSDKOPHIONI ENTEKNESKYCEPGLIPELIK LIKKEKESTRASETYLTIKELEVLI YI IRO
VCKYSDKOPHIONI ENTEKNESKYCEPGLIPELIK LIKKEKESTRASETYLLI YE ICYPLI A
CAMVITYLLCHKKNITK KEDEFSODAHIKLITKI ELEROYSASSESSINNSKIPELIY ZI IT
CAMVITYLLCHKKNITK KEDEFSODAHIKLITKI ELEROYSASSESSINNSKIPELIY ZI IT
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ASKORLEN LARREPGMEY SYDINKYPEEDOMTEKULYSCTYOLARGMEY LASOKCI
PASKORLEN LARREPGMEY SYDINKYPEEDOMTEKULYSCTYOLARGMEY LASOKCI
PASKORLEN LARREPGMEY SYDINKYPEEDOMTEKULYSCTYOLARGMEY LASOKCI
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HOSYWASGYLMAELTILGGSPYGLPYELFKLLKEGHRMDKPAMCTNELYMAMROC
HMAVPSGOPTFKOLVEDLDBILTITTNEEYLLLGGPLEOTSPSYDTRSSCSSGDEV
FSPERMYZECLEOYPHINGSYKT
1 609 c 660 g 339 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MVSWGRFICLVVVTMATLSLARPSFSLVEDTTLEPEEPPTKYQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="TK14 protein"
/protein_id="AAA61188.1"
/db_xref="GI:339711"
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99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2437; DB 9;
Pred. No. 0;
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752	TGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAGAAGGTTGCTTTGGG 1	1693	Qy
434	GCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTFCCA	1375	DЪ
692	CGGCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCAGAGGACCCAA	6	Qy
1374	CCAGC	1315	ρь
1632	CAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACACGCCTCTCTTC	1573	Qy
1314	GUTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTTTCGGCTGAG 1	26	Db s
3	CTGTGCACAAGCTGACCAAACCTATCCCCCTGCCCACACACA		0γ
2	ACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTCAGCAGCCAGC	1201	дb
51	CAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTCAGCAGCCAGC	1453	Qy
20			Db
5	ACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCCTGTATGGTGGTA	1393	Qγ
14	TCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATTACAGCTTCCCCA	1081	Db
ω 9	CTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATTACAGCTTCCCCA	1333	γO
80	TTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGGATATTCCTTTCAC	1021	Db
1332	TGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGGATATCCTTTCAC	1273	Qy
1020	ATATTCGGAATGTAACT	961	Db
1272	CCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACT	1213	οy
<u>6</u>		901	망
1212	GGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTCAAG	1162	οу
5	GTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAGTGGATCAAGCACGTGGAAAAG	841	Db
1161	TCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAGTGGATCAAGCACGTGGAAAAG	1102	Qy
840	ATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGAGACGCTAGAGTTT	781	Db
1101	TCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGAGACGTAGAGTT	1042	οy
œ	TACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGATCGCCTCACCGGCCC	721	Дb
1041	ACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGATCGCCTCACCGGCCC	982	Qy
N	ATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTATACCTGTGTGGTGGAGAATGAA	661	DЬ
981	TTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTATACCTGTGTGGTGGAGAATGAA	922	Qy
on .	AGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTC	601	DЪ
Ñ	AGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTC	862	Оу
0	TTTCGCTGCCCAGCCGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACCGGGAAG	541	DЬ
198	CGCTGCCCAGCCGGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAG	802	Qy
540	ACCAACACAGAAAAGATGGAAAAGCGGCTCCATGCTGTGCCTGCGGCCAACACTGTCAAG	481	Db
801	CCAACACAGAAAAAGATGGAAAAAGCGGCTCCATGCTGTGCCTGCGGGCCAACACTGTCAA	742	γQ
480	ACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGAGAG	421	рb
	ACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGAGCACCATACT	682	γQ
	ACTIGGTACTTCATGGTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGGATGAC	361	дb
681	ACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGGATG	622	Оу

	GCAGTGTTAAAACATGA	45	Вb
	CACATAAACGGCAGTGTTAAAACATG		9
2454	CATGCCTTACGAACCATGCCTTCCTCAGTAT	239	рь
2712	ATGATTCTGTTTTTTCTCCAGACCCCATGCCTTA	265	9
2394	5 CAACCTCTCGAACAGTATTCACCTAGTTACCCTGACACAAGAAGTTCTTGTTCTTCAGGA	233	DЬ
2652	AACCTCTCGAACAGTATTCACCTAGTTACCCTGACACAAGAAGTTCTTCTTCTTCAGG	259	οy
2334	5 GTAGAAGACTTGGATCGAATTCTCACTCTCACAACCAATGAGGAATACTTGGACCTCAGC	27	망
2592	TAGAAGACTTGGATCGAATTCTCACTCTCACAACCAATGAGGAATACTTGGACCTCAG	253	9
2274	5 ATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACGTTCAAGCAGTTG	ü	B
2532	SATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACGTTCAAGCAGTT	47	Qy
2214	5 AAGCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCCA	215	ď
2472	GCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCCAACTGCACCAACGAACTGTP	241	Qy
2154	AACT	209	В
2412	GGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCCGTGGAGGAACTTTT	235	Qy
2094	5 GCCCTGTTTGATAGAGTATACACTCATCAGGAGTGATGTCTGGTCCTTCGGGGTGTTAATG	203	DЪ
2352	CCTGTTTGATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTCGGGGTGTTAAT	229	8
	5 ATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGGATGGCTCCAGAA	197	Вb
2292	TAGACTATTAGAAAAAGACCACCAATGGGGGGCTTCCAGTCAAGTGGATGGCTCCAGAA		8
1974	AT-	-	D)
2232	AACAGAAAACAATGTGATGAAAATAGCAGACTTTGGACTCGCCAGAGATATCAACAAT	17	ş
1914	5 ATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCCAGAAATGTTTTG	85	В
2172	ATGGAGTACTTGGCTTCCCCAAAAATGTATTCATCGAGATTTAGCAGCCAGAAATGTTTTG	2113	Q
1854	5 CCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAGCTGGCCAGAGGC	179	рь
2112	CTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAGCTGGCCAGAGGC	205	οy
1794	GAATACCTCCGAGCCCGGAGGCCACCCGGGATGGAGTACTCCTATGACATTAACCGTGTT	1735	ф
2052	AATACCTCCGAGCCCGGAGGCCACCCGGGATGGAGTACTCCTATGACATTAACCGTGTT	199:	Qy
1734	TGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAAAGGCAACCTCCGA	1675	B
1992	TGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAAGGCAACCTCCGA	1933	Ŷ
1674	GAGATGGAGATGAAGATGATTGGGAAACACAAGAATATCATAAATCTTCTTGGAGCC	1615	Ор
1932	GAGATGGAGATGATGAAGATGATTGGGAAACACAAGAATATCATAAATCTTCTTGGAGCC	1873	9
1614	GTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAAGACCTTTCTGATCTGGTGTCA	1555	ф
1872	TGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAGAAGACCTTTCTGATCTGGTGTCA	1813	δ
1554	CAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCAAGGAGGGGGGTCACC	1495	Db
1612	CAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCAAGGAGGAGGCGTCACC	75	9
1494		1435	В

Job time : 7248 secs

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Title:
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1475-307 Million cell updates/sec
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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Scoring table: Searched: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

N\_Genesseq\_101002:\*

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| SIDD2/S SIDES/gogdata/geneseq/geneseqn-embl/MA1980.DAT:
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1689.6	1817.2	2188	2466	2670.4	3381	4268	4268	4268	Score
39.6	42.6	51.3	57.8	62.6	79.2	100.0	100.0	100.0	Query Match
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### ALIGNMENTS

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	20-SEP-2000;	20-SEP-2000;	20-SEP-2000;	18-SEP-2000;	18-SEP-2000;	05-JUN-2000;	05-JUN-2000;	0-MAY-2001	13-DEC-2001.	WO200194629-A2.	Homo sapiens	gene; ds.	ytostatic;	tomach; lu	uman; canc	and cancer	7007 - IVW- CT	 ABL64983;	BL64983 st	83		
							; 2000US-209473P.	30-MAY-2001; 2001WO-US10838.	•	-A2.	w.	The state of the s	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma.	stomach; lung; prostate; pancreas; carcinoma, antitimon; carcinoma	Human; cancer; colon; breast; ovarv; opsophagus; kidney; thuroid;	many cancer related gelle sequence SEQ ID NO:3320.	(first entry)		ABL64983 standard; DNA; 4268 BP.			

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27-SEP-2000;
28-SEP-2000;
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28-SEP-2000;
                                                                                                              The present invention describes a method (Mi) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gone (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in Millisto OABL/OIID), or is at least 5% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostanic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, cosponageal, ovarian, kidney, prostate or pancreatic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening for anti-neoplastic agent involves exposing cells chemical agent to be tested for anti-neoplastic activity, are determining a change in expression of a gene of a signature
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CCCAAGGACCACTCTTCTGCGTTTGGAGTTGCTCCCCACAACCCCGGGCTCGTTGCCTTTC

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Sequence

4268

BP; 1199 A;

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infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour. adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,

Matches 4268;

Local Similarity

100.0%; llarity 100.0%; Conservative

Score 4268; brad. No. 0; C; 1028 G; 1077

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Mismatches

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OY 2161 AGAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGACTTTGGACTCG
Oy 2101 CTGGCCAGAGGCATGGAGTACTTGGCTTGCCAAAAATGTATTCATCGAGAT    1
Oy 2041 ATPANCEGRETTICSTGANGANG-ACATGANCETTCANGGACTTGGTGTGTTANG Db 2041 ATPANCEGRETTICSTGANGGANGCANTGANCETTCANGGANCTTGGTGTCATG
OY 1981 GGCAACCTCCGAGATACCTCCGAGCCCGGAGGCCACCGGGATGGAGTAC
OY 1921 CTTCTTGGAGCCTCCACACAGATGGGCCTCTGTATGTCATAGTTGAGTATAGT Db 1921 CTTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATA
18
OY 1741 GTTGCTTTGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAGG Db 1741 GGTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAG Db 1741 GGTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAG
1681 GAGGACCCAAAATGGAGTTT
162
Oy 156 GTTTCGGCTGAGTCCAGCTCCTCATGAACTCCAACACCCCGCTGGTGAGC  Db 1561 GTTTCGGCTGAGTCCAGCTCCATGAACTCCAACACCCCCGCTGGTGAGCCCCCGCTGGTGAGCCCCCGCTGGTGAGCCCCCGCTGGTGAGCCCCCCGCTGGTGAGCCCCCCGCTGGTGAGCCCCCCGCTGGTGAGCCCCCCGCTGGTGAGCCCCCCCTGGTGAGCCCCCCGCTGGTGAGCCCCCCGCTGACACACCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCTGGTGAGCCCCCCCC
OY 1501 AGCAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAG
Oy 1441 TGTATGGTGGTAACAGTCATCCTGTGGCGAATGAAGAACACGACGACGAAGAA 
Oy 1381 ACACCTTCCCCAGACTACCTGGACATAGCCATTTACTGCATAGGGCTCTTT Db 1381 ACACCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGCTTTTCTCTTACTGCATAGGGCTTCTTT
Oy 1321 ATATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGGGCCTGGAAGAG
OY 1261 CGGAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTC
OY 1201 AAGGTTCTCAAGGCCCCCGGTGTTAACACCACGACAAAAAAATATAAGGCCGCGACAAAAAAAA
OY 1141 TGGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGC

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                           Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
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  Claim 1;
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human: cancer: colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
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                                                                                                                     AGTAGGACTGTAGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCA 660
                                                                                                                                                                                         GAGTACTTGCAGATAAAGGCCCCCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCC
                                                                                                                                                                                                                                 GAGTACTTGCAGATAAAGGGCGCCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCC
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                                 TCCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGGAACAGTAAC 720
                                                                                          AGTAGGACTGTAGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCA
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100.0%; Pred. No. 0
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1860	301 GAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCCACAGAGAAAGACCTTTCT :	0у 18
1800	41 GGTTGC	
1800	41 GGTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCC	
74	B1 GAGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAGAGCCCCTGGGAGAA	<u>_</u>
7	81 GAGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAGAA	_
1680	21 CGCCTCTCTCAACGGCAGACACCCCCATGCTGGCAGGGTCTCCGAGTATGAACTTCCA	Db 16
œ	21 CGCCTCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCC	μ.
62	61 GTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA	
N	61 GTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA	
on o		
Ö.	01 AGCAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAA	_
1500	* 1 TUTATUGTUGTAACKSITCATCCTGTGCGGAATGAAGACACGACCAAGAAGCCAGACTTC  41 TGTATGGTGGTAACAGTCATCCTGTGCGGAATGAAGAACACGACCAAGAAGCCAGACTTC  41 TGTATGGTGGTAACAGTCATCCTGTGCGGAATGAAGAACACGACCAAGAAGCCAGACTTC	Db 14
1440	81 ACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCC	
1440	81 ACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGC	
1380	321 ATATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATT	_
1380	ATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAC	Qy 1:
w	261 CGGAATGTAACTTTTGAGGAACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGG	<u> </u>
32	61 CGGAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATT	_
26		Db 1:
σ.	01 AAGGTTCTCAAGGCCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTCT	_
0	141 TGGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTC	_
0	41 TGGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCC	و
14	081 GTCGGAGGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAG	-
1140	TCGGAGGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGGCCCCACATCC	Qy 1
9	021 GAGCGATCGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTG	
108	21 GAGCGATCGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGC	Qy 1
10	961 ACCTGTGTGGTGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTG	Db
10	61 ACCTGTGTGGTGGAGAATGAATACGGGTCCATCAATCACACGTA	٧
6	901 CGAAACCAGCACTGGAGCCTCATTATGGAAAAGTGTGGTCCCATCTGACAAGGGAAATTAT	ъ
	01 CGAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATT	¥
ō	41 CGGTGGCTGAAAAACGGGAAGGAGTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGT	-
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4 .	781 CCTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGAACCCAATGCCAACCATG	•
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780	AGCACCATACTGGACCAACACAGAAAAGATGGAAAAGCGGCTCCATGCTG	Qy

2940	ATGTGTAAAGATTTATACAGTTGAAAACTTGTAATGTTCCCCA	288	5
2880 2880	TCCACTTGTATATATGGATCAGAGGAGTAAATAATTGGAAAA 	282	ρ δ
2820 2820	GGAACCTAGCTACACTGAGCAGGAGAC 	276: 276:	P 6
2760 2760	ACGGCA ACGGCA	270: 270:	δ 5
2700 2700	TTCTTCAGGAGATGATTCTGTTTTTTCTCCAGACCCC	264	유 5
2640 2640	TGGACCTCAGCCAACCTCTCGAACAGTATT 	258: 258:	B S
2580 2580	GTTGGTAGAAGACTTGGATCGAATTCTCACTCTCACA 	2521	99 99
2520 2520	AACGAACTGTACATGATGATGAGGGACTGTTGGCATGGAGTGCCCTCCCA	2461 2461	용 성
	. GAGGAACTTTTTAAGCTGCTGAAGGAAGGACACAGAATGGATAAGC 	4 4	A 6
2400 2400	GGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGCTCGCCCTACCCAGG	2341	g 9
2340 2340	ATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTG	2281 2281	유 왕
2280 2280	GATATCAACAATATAGACTATTACAAAAAGACCACCAATGG(	N N	ρ δ
2220 2220	agaaatgttttggtaacagaaaacaatgtgatgaaatagg 	2161 2161	P 6
2160 2160	TICA TICA	2101	₽ 5
2100 2100	ATTANCCGIGTICCIGAGGAGCAGAT	2041	P 6
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1980 1980	CTPCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATA	1921 1921	용 성
1920 1920	GATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGAAA	96	8 8
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stomach; lung; prostate; pancreas; carcinome; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcin
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### Young PE, Soppet DR, Augustus M, Weaver Z;

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Screening for anti-mapplastic agent involves exposing calls to a chamical agent to be tested for anti-mapplastic activity, and determining a change in expression of a gene of a signature gene set WPI; 2002-188264/24

Claim 1; SEQ ID 6931; 44pp; English

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be fested for anti-neoplastic activity, determining a change in comprises a sequence (5) selected from 647 sequences (given in ABC1664 comprises a sequence (5) selected from 647 sequences (given in ABC1664 comprises a sequence (5) selected from 647 sequences (given in ABC1664 comprises a sequence (5) selected from 647 sequences (given in ABC1664 comprises a sequence (5) selected from 647 sequences (given in ABC1664 comprises a sequence (5) selected from 647 sequences (given in ABC1664 comprises in ABC1664 comprises in Sequences (given in ABC1664 comprises in ABC1664 comprises in Sequences (given in ABC1664 comprises in A carcinoma, papillary carcinoma and Wilm's tumour.

Sequence 4268 BP; 1199 A; 964 C; 1028 G; 1077 T; 0 other;

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Best Local Similarity
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                                                                                                                                                                                                                                               1 CCCAAGGACCACTCTTCTGCGTTTGGAGTTGCTCCCCACAACCCCGGGCTCGTCGTTTC
CTGGTCGTGGTCACCATGGCAACCTTGTCCCTGGCCCGGCCCTCCTTCAGTTTAGTTGAG
                         TATGGAAGAGGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGC
                                         TATGGAAGAGGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGC
                                                                           TIGGGGGTAGTCCATGCCCGTAGAGGAATGTGCAGATGGGATTAACGTCCACATGGAGA
                                                                                                                                                     AAGTCACTGCAGCAGCAGCGGCAGCGCCTCGGTTCCTGAGCCCCACCGCAGGCTGAAGGCA
                                                                                                                              AAGTGACTGCAGCAGCGGCAGCGCCTCGGTTCCTGAGCCCACCGCAGGCTGAAGGCA
                                                                                                                                                                                TCCATCCCGACCCACGCGGGGCCGCGGGGACAACACAGGTCGCGGAGGAGCGTTGCCATTC
                                                                                                                                                                                                                                 CCAAGGACCACTCTTCIGCGTTTGGAGTTGCTCCCACAACCCCGGGCTCGTCGCTTTC
                                                                                                                                                                                                                                                                                       Conservative
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1440	ACAGCTTCCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCC	1381	γo
1380	TATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGAT	1321	DЬ
1380	ATATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATT	1321	Q
1320 1320	CGGANTGTAACTTTTGAGGAGCTGGGGGATNTACGTGCTTGGGGGGTAATTCTATTGGG	1261 1261	Db 03
1260	ARGGTTCTCAMGGCCGCCGGTGTTAMCACCGGGACAMAGAGATTGAGGTTCTCTATATT AAGGTTCTCAAGGCCGCCGGTGTAAAAACACCACGGACAAAGAGATTGAGGTTCTCTATATT	1201	B 6
ט ע	GGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGCCCCGACGGGCTGCCCTACCT	س; ر	}
N	GCCCTACC	1141	Q
1140	GTCGGAGGAGACGTYGTTGCTGCAAGGTTTACAGTGATGCCCAGCCCCACTCCAG 	1081	Db 04
. 08	AGCGATCGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTG	02	Db
80	GCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTG	1021	Qy
1020	TGTGGTGGAGAATG	ō	В
1020	CCTGTGTGGGGGGAAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGT	961	ý
960	CATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAAT	901	DЬ
960	GAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTA	901	Ŷ
900	CGTTGCTGAAAACGGGAAGGAGTTTAAGCAGGACTATCGCATTGGAGGCTACAAGAGTA 	841	P 29
840	CTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGGAACCCAATGCCAACCATG	781	В
840	CGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGGGAACCCAATGCCAACCATG	781	9
780	CGGCTCCATGCTGTG	721	D
780	ACAAGAGAGCACCATACTGGACCAACACAGAAAAGATGGAAAAAGCGGCTCCATGCTGTG	721	γQ
720	TGCGGAAGATTTTGTCAGTGAGAACAGTAAC	661	₽
720	CCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAAC	661	γo
660	GTAGGACTGTAGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCA	601	망
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600	AGTACTTGCAGATAAAGGGCGCCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCC	541	o,
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540	TCAGTTGGACTAAGGATGGGGTGCACTTGGGGCCCCAACAATAGGACAGTGCTTATTGGG		δ
480	TAGGTGCCTGCCAGGGAGTCCTAGAGGTGCCTCTTGTAAAGATGCCGCCGTGTG1111111111	421 421	B 8
420	TTAGAGCCAGAAGCAACCAAATACCAAATCTCTCAACCAGAAGTG	361	Db
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AACGAACTGTACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACG	GAGGACTTTTTAACCTGCTGAACGAAAGGAAAAGAATGAAT	GGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCGTG	TRESCRICADANGECTETTTGATAGAGTATACACTATECAGAGTGATGCTGGGTCCTTC	GATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGGGGGTTCCAGTCAATGGGGGGGTTCAGTATAGGATATTAGAAAAAGACCACCAATGGGGGGGTTCCAGTCAAGTGGGATATTACAAAAAAGACCACCAATGGGGGGGTTCCAGTCAAGTGG	AGAAATGTTTTGGTAACAGAAAGAATGTGATGAAAATAGCAGACTTTGGACTCGCCAGA	CTOGCCEAGAGCATGGAGTACTTGGCCTTCCCAAAATGTATTCATGGAGATTTAGGGCCCCCCTTGGCCAAAATGTATTCATGGAGATTAGTCATGCAGCCCCCAAAAATGTATTCATCGAGAATTTAGCAGCCCCCCAAAAATGTATTCATCGAGAATTTAGCAGCCCCCCCC	ATTANCOGTETTCCTGAGGAGAGATAGACCTTCAAGGACTTGGTGTCATGCACCTACCAGAGAAGAAGAAGAAGAAGAAGACCTTCAAGGACTTGGTGTCATGCACCTACCAGAGAGAAGAAGAACCTTCAAGGACTTGGTGTCATGCACCTACCAGAGAGAG	GCCANCUTCGAGATACCTCCGAGCCCGCAGCCACCGGAGGGATACTCCTATGAC 2	CTTCTTGGAGCCTGCACACAGATGGCCTCTCTATGTCATAGTTAGATATGCCTCTAAA  [	GATCTGGTGTCAGAGATGAGAGATGATGAAGATGATTGGGAAACACAAGAATATCATAAT 1 	GAGGCGGTCACCGTGAAGATGTTGAAAGATGCCACAGAGAAAGACGTTTCT 1	GCTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCAAG   GCTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGACCAAG 	LABGARCEANANTGGBAGTTTCCAAGAGTAACTTGACATGGGCAAGCCCTTGGGAAA   LAGAGACCAAAATGGBAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCTTGGAAAA   GAGGACCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAAAA	COCCTCTCTTCAACGCAGACACCCCATGCTGGCAGGGTCTCCGAGTATGACACTTCCA 	GTTTCGCCTGAGTCCACCCACAACTCCACACCCCCCTCGTGAGGATAACAACTCCGCTGGTGAGGATAACAACTCCTCTTCACACACTCCACCCCCCTGGTGAGGATAACAACACACAC	ACCACCACCCCCTTTCCACAAGCTGACCAACCTATTCCCCCTTCCGAGACAGGTAACA   ACCACCACCCCCTTTCCACAAGCTGACCAAACGTATCCCCCTGCGAGACAGAGAAGAAGAAACAAAACATATCCCCCTGCGAGACACAGAGACAACAAAACATATCCCCCTGCGAGACACAGAGAACAACAAACA	TETATIGETGETAACAGTCATCCTGTGCCGAATGAACAACACGACAAGAACCAGACTTC 1111111111111111111111111111111111	ACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCC 1
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160	541 TTGTGTTTAAATGCTGCTGTCAGACGATTGTTCTTAGACCTCCTAAATGCCCCCATATHS 541 TTGTGTTTAAATGCTGCTGCTGCAGACGATTGTTCTTAGACCTCCTAAATGCCCCCATATHS 541 TTGTGTTTAAATGCTGCTCATCAGACGATTGTTCTTAGACCTCCTAAATGCCCCCATATHS
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3480 3480	3421 ATGCAGGCAGCAGAGAGAGATAGTTAATCTATTGCTTGGACTTAACTAGTTATCAGATCC   1
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3360 3360	3901 GAGGTGGAAAATACTTTTGCTTTCAGGAAAATGGTATAACGTTAATTAA
3300	3241 TTTTANTACCTATTTCCTAAATGCTGTTCTTAGACATAATTTCTTAATTTTCACCGAGCA
3240 3240	3181 TATTTTTGTATTGATTTAAATGGATGTCCCAATGCACCTAGAAAATTGGTCTCTCTTT 
3180 3180	3121 TGGATGTAGGAAATGAGTGAATGATGTAFAAAGATGTAGTATGATGTTAGAAGGAGT
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3060 3060	3001 GCTGTGGACCAGTAGGACTCAAGGTGGACGTGCGTTCTGCCTTCCTT
3000	2941 TCTGGAGCAGTGCGACTGCCACAAGCCACCATGTAAGCCCTCTCACCTGCGCTGCGGTTCTG
2940 2940	2881 TATGTGTAAAGATTTATACAGTTGAAAACTTGTAATCTTCCCCAGGAGGAGAAGAAGGGTT
2880 2880	2821 TTGTTGTCTCCACTTGTATATATGGATCAGAGGAGTAAATAATTGGAAAAGTAATCAGCA 
2820 2820	2761 CAAACAGGAGCACTGGGAACCTAGGTAGATGAGCAGGGAGACCATGGCTCCCAGACC
2760 2760	2701 CCTCAGTATCCACACATAAACGGCAGTGTTAAAACATGAATGA
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2640 2640	2581 TYGGACCYAGCCAACCITYGGAACAGTATTCACCTAGTTACCCTGGAACAAGAAGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The cDMA sequence was obtd. by screening a one day old human brain strain (stem cDMA library in lambda gill with an antisense 33 base oligomer (CI stem cDMA library in lambda gill with an antisense 33 base oligomer (CI stem cDMA library in lambda gill with an antisense 33 base oligomer (CI stem cDMA library in lambda beta to restream the library. Will 37 cells were cottamsfected with a 1:20 mixture of psylmoe and the CI cells were cottamsfected with a 1:20 mixture of psylmoe and the CI bek expression vector conty, the bek probe inserted into pw330 canhancer. Clones of bek transfected cells have increased binding CI for aFGF receptors, the best being clone bhack which was used for CI of aFGF receptors, the best being clone bhack which was used for CI of aFGF receptors, the best being clone bhack which was used for CI of aFGF receptors. The best being clone bhack which was used for CI of aFGF receptors proteins enough by the which was used for CI of a FGF receptor protein may not compans. to inhibit undesirable heparing the used in pharmaceutical compans. to inhibit the CI binding of an opportunistic pathogen to human cells. Such undesirable CC tastlone may a lao be used for screening drugs.

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DB; AAR20750.
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GCCCAACAATAGGACAGTGCTTATTGGGGAGTACTTGCAGATAAAGGGCGCCACGCCTAG
                                                                                                                                                                                        CAAATACCAAATCTCTCAACCAGAAGTGTACGTGGCTGCGCCAGGGGAGTCGCTAGAGGT
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Pred. No. 0;
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193 GAAAATAGCAGACTTTGGACTCGCCAGAGATATCA 	B 8
133 AAAATGTATTCATCGAGATTTAGCAGCCAGAAATGT: 	. Q
2073 CANGANCTYGGTGTCAPGCACCTACCACTGGCCAGAGGCATGGAGAGACTACTGGCCTTCCCA	B 64
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1713 GETGACACTGGGCAAGCCCCTGGGAGAGGTTGCTTTGGGCAAGTGGTGCTGGAGAGC 1111 GETGACACTGGGCAAGCCCCTGGGAGAGAGCTTGCTTTGGGCAAGTTGGTCATGGCGGAAGC 1610 GCTGACACTGGGCAAGCCCCTGGGAGAAGATGCTTTGGGCAAGTGGTCATGGCCGAAGC	Db Qy
1653 GGCAGGGGTCTCCGAGTATGAACTTCCAGAGGACCCAAAATGGGAGTTTCCAAGAGATAA 	Db Oy

ABL61834 standard; DNA; 3244 BP

15-MAY-2002 (first entry)

ABL61834;

Colon adenocarcinoma related gene sequence SEQ ID NO:171.

RESULT 5
ABLGE 18
ABL Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach, lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; gene; ds.

Homo sapiens

WO200194629-A2.

13-DEC-2001.

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expression is indicative of anti-neoplastic activity. (I) has evicatantic activity and can be used in gene therapy. All can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collecte with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. All can be used in the treatment of concer such as colon, breast, stomach, lung, thyroid,
                                                                                                                                                The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a change in agent to be tested for anti-neoplastic activity, determining a change in agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447-sequences (given in ABAG1664 to ABL70110), or is at least 55% identical to (S), where a change in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANGTGACTGCAGCAGCAGCGCCAGCGCCTCGGTTCCTGAGCCCACCGCAGGCTGAAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGTGACTGCAGCAGCAGCGCCAGCGCCTCGGTTCCTGAGCCCACCGCAGGCTGAAGGCA
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                                           CGGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTA
                                                                                                      CCTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGAACCCAATGCCAACCATG
                                                                                                                                   CCTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGAACCCAATGCCAACCATG
                                                                                                                                                                                                AACAAGAGGAGCACCATACTGGACCAACACAGAAAAGATGGAAAAGCGGCTCCATGCTGTG
                                                                                                                                                                                                                                                                                        AGTAGGACTGTAGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCA
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                                                                                                                                                                   AACAAGAGAGCACCATACTGGACCAACACAGAAAAGATGGAAAAGCGGCTCCATGCTGTG
                                                                                                                                                                                                                             TCCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAAC
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Pred. No. 0;
0; Mismatches
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CGAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTAT

	1906	7 GGCAACCTCCGAGAATACCTCCGAGCCCGGAGGCCACCCGGGATGGAGTACTCCTATGAC	184	D
	2040	1 GGCAACCTCCGAGAATACCTCCGAGGCCGGGAGGCCACCCGGGATGGAGTACTCCTATG	198	9
	1846	7 CT	178	Db
-	1980	TTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCT	192	Qy
	1786		7	문
-	3	ATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGGAAACACAAACAA	186	Q
0	1860 1726	LANGUGETLACCOTTGCCCGTGAAGATGTTGAAGATGATGCCACAGAGAAGACCTTTCT	166	B 4
0,	1666	7 GGTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCAAG	o o	9
_	1800	41 GGTTGCTTTGGGCAAGTGGTCATGGCGAAGCAGTGGGAATTGACAAAGACAAGCCCCAAG	. 7	Ϋ́
	1606	47 GAGGACCCAAAATGGGAGTTTCCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAGAA	15,	DЬ
_	1740	AGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAC	161	Q
•	in	87 CGCCTCTCTCAACGGCAGACACCCCCATGCTGGCAGGGTCTCCGAGTATGAACTTCCA	14:	Dβ
_	1680	GCCTCTCTTCAACGGCAGACACCCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCC	16:	Qy
٠.	4.8	27 GTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA	14:	DЬ
_	1620	TTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAAC	15	γo
٠.	1426		14:	В
_	1560	01 AGCAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGT	15	Qy
01	1426	27	14	망
0	1500	41 TGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGC	14	Qy
o,	1426	.27	14	Db
J	1440	81 ACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGC	13	VQ
U)	1426	27	14	Db
0	1380	21 ATATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGAT	13	γQ
U1	1426	.27	14	Db
J	1320	61 CGGAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATT	12	VQ
U1	1426	15 AAGGTTCTCAA	14	밁
J	1260	201 AAGGTTCTCAAGGCCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTCTATATT	12	γo
-	4		13	Дb
0	1200	41 TGGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCT	11	οy
		95 GTCGGAGGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAG	12	밁
0	1140	81 GTCGGAGGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCC	10	9
	1080	211 GAGCGATCGCCTCACCGGCCATCCTCCAAGCCGGCACTGCCGGCAAATGCCTCAAGGG 111111111111111111111111111111111	10	р Q
4	1234	/3 ACCITIGETGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTG	-	5
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3180	GGATGTATGTAAATATATTCAAATTATGTATAAATATATAT	3121	Qy
2986	TAATTGGAGAAGATTTATGTCAGCACACACTTACAGAGCACAAATGCAGTATATAGGTGC		망
3120	AATTGGAGAAGATTTATGTCAGCACACACTTACAGAGCACAAATGCAGTATATAGGTG	0	Оу
2926	GCTGTGGACCAGTAGGACTCAAGGTGGACGTGCGTTCTGCCTTCCTT	2867	ф
3060	CTGTGGACCAGTAGGACTCAAGGTGGACGTGCGTTCTGCCTTCCTT	3001	Qγ
2866	TCTGGAGCAGTGGCACAAGCCACCATGTAACCCCTCTCACCTGCCGTGCGTTCTG	ω v	Db 4
80	HIGH STRUMENT THE FACHET GARAGETT GTARTETT FOR CONTROL TO THE CONTROL THE CONTROL TO THE CONTROL THE CONTROL TO THE CONTROL TH	٥ ،	Q (
94	TATGTGTAAAGATTTATACAGTTGAAAACTTGTAATCTTCCCCAGGAGGAGGAAGAAGGTT	2881	P 29
7	TGTTGTCTCCACTTGTATATATGGATCAGAGGAGTAAATAATTGGAAAAGTAATCAGCA	2687	В
2880	GTTGTCTCCACTTGTATATATGGATCAGAGGAGTAAATAATTGGAAAAGTAATCAG		0y
68	CAAACAGGACAGCACTGGGAACCTAGCTACACTGAGCAGGAGACCATGCCTCCCAGAGC	2627	DЬ
2820	AAACAGGACAGCACTGGGAACCTAGCTACACTGAGCAGGGAGACCATGCCTCCCAGA	2761	Оу
	CCTCAGTATCCACACATAAACGGCAGTGTTAAAACATGAATGA	2567	Db
2760	CTCAGTATCCACACATAAACGGCAGTGTTAAAACATGAATGA	2701	Qy
2566	TGTTCTTCAGGAGATGATTCTGTTTTTTCTCCAGACCCCATGCCTTACGAACCATGCCTT	2507	Дb
2700	CTTCAGGAGATGATTCTGTTTTTTCTCCAGACCCCATGCCTTACGAACCATGC	2641	ν
2506	TTGGACCTCAGCCAACCTCTCGAACAGTATTCACCTAGTTACCCTGACACAAGAAGTTCT	2447	DЬ
-	GGACCTCAGCCAACCTCTCGAACAGTATTCACCTAGTTACCCTGACACAAGAAGTTC	2581	Qy
2446		ü	Db .
n o	AAGCAGTTGGTAGAAGACTTGGATTGGATTTGTOTOTOTOTOTOTOTOTOTOTOTOTO	Ġ.	Oy Y
38	ANCGAACTGTACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACG	ũ	Дb
52	GAACTGT ACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAAC	2461	Qγ
32		2	망
6	AGGAACTTTTTAAGCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCC	2401	γo
Ñ	GGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCCGTG	2207	Db
2400	GGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCCTCGCCCTACCCAGGGATTCC	2341	Qy
20	ATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTC	2147	Db
2340	TGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGATGTCTGGTC	2281	Оу
14	GATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGG	2087	Db
2280	ATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTG	2221	Qγ
8	GAAATGTTTTGGTAACAGAAAACAATGTGATGAAAAATAGCAGACTTTGGACTCGCCAGA	0	Db
22	GAPATGTTTTGGTAACAGAPAACAATGTGATGAPAATAGCAGACTTTGGACTCGCCA	-	Qy
02	TIGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCC	1967	DЬ
9	TGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAG	_	Οy
96	ATTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCCACC	1907	Db
2100	TTAACCGTGTTCCTGAGGAGGAGGATGACCTTCAAGGACTTGGTGTGATGCACCTACCA	2041	Qy

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RESULT 6
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                                    The invention relates to a method for inhibiting expression of a target gene (AB191658-AB191797) in a cell by introducing at least one old old provides the standard of the consisting of at most 49 sequential nucleotide pairs, with at least one end a complementary with the target gene and has at least one end a single-strended segment of 1-4 nt. The method provides single-strended segment of 1-4 nt. The method provides described to the strended segment of 1-4 nt. The method provides described against genes present in pathogens (e.g. Plasmodium or virusss/viroids, pathogenic on humans, animals or plants) or against cycokine, id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, HTV, HCV. gene expression; oligoribonucleotide: tumour; pathogen;
Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
cytostatic; virucide; profozoacide; antibacterial; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JAN-2001; 2001DE-1000586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL91742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL91742 standard; DNA;
                                                                                                                                                                                                                                                   Claim 13; Page 59; 104pp; German.
                                                                                                                                                                                                                                                                                              Inhibiting gene expression in cells, useful for e.g. treating tumors,
by introducing double-stranded complementary oligoRNA having unpaired
                                                                                                                                                                                                                                                                                                                                         WPI: 2002-270454/32.
                                                                                                                                                                                                                                                                                                                                                                                                (RIBO-) RIBOPHARMA AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTAATAGCTATTTGCTAAATGCTGTTCTTACACATAATTTTCTTAATTTTCACCGAGCA 3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGTAATATACAAAACAA 3244
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                              and
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                            intracellular concentration.
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Sequence

2466 BP;

671 A;

604 C;

656 C;

535 T; 0 other

CATGGTTGACAGTTCTG 1353	4 ACGTGCTTGGCGGGTAATTCTATTGGGATATCCTTTCACTCTG	у 129
GGACGCTGGGGAATAT 10	CAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACTTTTC	96
AGGACGCTGGGGAATAT 1293	ACAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACTTTTC	123
CCGTGTTAACACCAC	GGCCGACGGGCTGCCCTACCTCAAGGTTCTCAAGGCCG	90
CCGGTGTTAACACCACG 1233	TACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTCAAGGCCC	_
)AAAAGAACGGCAGTAAA 900	TACAGTGATGCCCAGCCCCACATCCAGTGGATCAAGCACGTGGAAAAGA	Db 841
ACGGCAG	TACAGTGATGCCCAGCCCCACATCCAGTGGAT	
AGTTTGTCTGCAAGGTT 840	GGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGAGACGTAGAGTTT	Db 781
AGTTTGTCTGCAAGG	TGCCGGCAAATGCCTCCACAGTGGTCG	10
GGCCCATCCTCCAAGCC 780		7
GCCCATCCTCCAAGC	acacgtaccacctggatgttgtggagcgatcgcctcacc	99
AATACGGGTCCATC 72	GTGGTCCCATCTGACAAGGGAAATTATACCTGTGTGGTGGAGAATC	Db 661
тса апассистскатс 9	TO CONTROLLO DE LA CONTRA PER CACOLOCA CACOLOCA CONTRA LA CONTRA CACOLOCA C	3 :
GCCTCATTATGGAAAGT 933 	GAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAG 	•
GAAGGAGTTTAAGCAG 60	CGGGGGAACCCAATGCCAACCATGC	٠ س
7	GCCGGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGG	Оу 814
ccc	CATGCTGTGCCTGCGGC	4
CAACACTGTCAAGTTTCGCTGCCCA 813	AAGATGGAAAAAGCGGCTCCATGCTGTGCCTGCGGCCAACACTGT	ОУ 754
ACTGGACCAACACAGAA /53 	GANGATTTTGTCAGTGAGAACAGTAACAAGAGAGGCCCATACTGGACCAACAC  [	Qy 694 Db 421
TGCG 42	GGTGAATGTCACAGAT	ω
HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ATGGTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGGA	0у 634
STGAAACTTGGTACTTC 360	TTGTACTGCCAGTAGGACTGTAGAC	ω
AGTGAAACTTGGTACTTC 633	ACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAGAC	Оу 574
CTAG	CTTATTGG	N
AGGGCGCCACGCCTAGA 573		v
ດ-	CGCTGCCTGTTGAAAGATGCCGCCGTGATCAGTTGGACTAAGGA	·
GGACTAAGGATGGGGTGCACTTGGGG 513	GCTGCCTGTTGAAAGATGCCGCCGTGATCAGTT	Qy 454
GGAGTCGC	AAATACCAAATCTCTCAACCAGAAGTGTACGTGGCTGCGCCAGG	,
GGGAGTCGCTAGAGGTG 453	TCTCAACCAGAAGTGTACGTGGCTGCGCCAC	Оу 394
GCCAGAAGAGCCACCAACC 120	GCCCGGCCCTCCTTCAGTTTAGTTGAGGATACCACATTAGAGCC	-
CACCAACC 3	CCCTCCTTCAGTTTAGTTGAGGATACCACATTAGA	Оу 334
ATGCAACCTTGTCCCTG 333 	ATGGTCAGCTGGGTCGTTTCATCTGCCTGGTCGTGGTCACCATC	Oy 274 Db 1
ls 0; Gaps	al Similarity 100.0%; Fred. NO. 0; 2466; Conservative 0; Mismatches 0	Matches
Length 2466;	57.8%; Score 2466; DB 2	ne e

2433	GGCTGGCCCTACCCAGGGATTCCCGTGGAGGAACTTTTTAAGCTGCTGAAGGAAG	2374	õ
2373	ACTARCAGAGTGATGTCTGGTCCTTCGGGGTGTTAATGTGGGAGAGTCTTCACTTTAGG 2	2041	B &
2313	ACCANTGGCGGCTTCCAGTCANGTGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATAC	19	B 8
2253 1980	AAAATAGCAGA                AAAATAGCAGA	19	B 0
2193 1920	AANGETATTCATCGAGATTTAGCAGCAGAAAGTTTTTGGTAACAGAAAAAATGTTTTGGT 	18	B 6
2133	AAG	18	p Q
2073	COACCCGGGATGGAGTACTCCTATGACATTAACCCTGTTCCTGAGGACCAGATGACCTTCCTIIIIIIIIII	17	P Q
2013 1740	PATGTCATAGTTGAGTATGCCTCTAAAGGCAACCTCCGAGAATACCTCCGAGCCCGGAGGCCCGGAGGCLLLLLLLLLL	16	D Q
19 <b>5</b> 3 1680	ATTGGGAMACACAAAAATATCATCATCATCTTGGAGCCTGCACACAGGATGGGCCTCTCTCT	16	g g
1893 1620	GATGATGCCACAGAGAAAGACCTTTCTGATCTGGTGTCAGAGATGGAGATGATGAAGATG 	18	B 6
1833	GGGANTTGACAAGACAAGCCCAAGGAGGGGTCACCGTGGCCCTGAAGATGTTGAAA 	15	B 8
1773 1500	CTGRCACTGGGCAAGCCCCTGGGAGAAGGTTGCTTTGGGCAAGTGGTCATGGCGGAAGCA		- B - 6
1713 1440	CAGGGGTCTCCGAGTATGAACTTCCAGAGGACCCAAAATGGGAGTTTCCAGAGATHIH 	138	B &
1653 1380	ACACCCCGCTGGTGAGGATAACAACACGCCTCTCTTCAACGGCAGACACCCCCATGCTG	132	D 40
1593 1320	4 OGTATCCCCCTGCGGAGACAGGTAACAGTTTCGGCTGAGTCCAGCTCCATGAACTCC	153	유왕
1533 1260	A NGANGKGAGCAKGAAGCCAGACTTCAGCAGCCGGCCGTTTGCACAAGCTGACCAAA 	ь v	B 8
1473 1200	TGCATAGGGTCTTCTTAATCGCCTGTATGGTGGTAACAGTCATCCTGTGCCGAATG 	11 14	B 8
1413 1140	1 CCAGCGCTGGAAGAGAAAAGGAATTACAGCTTCCCCAGACTACCTGGGAGTAGCCATT 	у 135 ъ 108	B 8
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RESULT 7
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A cDNA library prepared from human cancer cell line Kato III mRNA was screened with an oligonuclectide corresponding to amino acids 529-541 of chicken basic FGF receptor. Three positive clones were obtained. One was cloned into pUCl18/119 to give pTB1229 (see
                                                                                                                                                                                   28-DEC-1990;
27-APR-1990;
31-JUL-1990;
14-SEP-1990;
                                                     Example 3;
                                                                    New mutein(s) of proteins with fibroblast growth factor receptor activity, useful for treating multiple endocrine neoplasia, prostatic hypertrophy, used for diagnosis
                                                                                                                WPI; 1991-353723/48.
P-PSDB; AAR15268.
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                                                     Fig 7; 88pp;
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90JP-0113146.
90JP-0204438.
90JP-0245256.
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8200000 8800000 B õ 밁 ş 밁 ş 밁 ş 망 Š 밁 ş õ 밁 Š B Q DЬ õ В Š В δÃ 밁 Ş 밁 Ş 밁 á 망 9 Query Match Best Local Matches 2259; AAQ14849). The complete FGF coding sequence was obtained by ligating the insert from pTB1229 to the DNA sequence of the plasmid pTB1281 insert which encodes the carboxyl terminus of the FGF receptor from Glu 533 onwards. 1150 Sequence 2676 BP; 743 A; 645 C; 738 G; 550 T; 1090 841 781 1030 721 970 661 910 601 .50 541 790 481 730 421 670 361 610 301 550 241 490 181 430 121 370 310 61 Loca l GCACCATACTGGACCACAGAAAAAGATGGAAAAGCGGCTCCATGCTGTGCCTGCGGCC 789 GATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGA 480 GATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGA 729 GTAGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCATCCGGAGAT 420 CAGATAAAGGGCGCCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACT CAGATAAAGGGCGCCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACT 609 GCGCCAGGGGAGTCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCGCCGTGATCAGTTGG GCGCCAGGGGAGTCGCTAGAGGTCGCGCTGCCTGTTGAAAGATGCCGCCGTGATCAGTTGG 489 TTAGAGCCAGAAGAGCCAACCAACCAAATACCAAATCTCTCAACCAGAAGTGTACGTGGCT 180 TTAGAGCCAGAAGAGCCAACCAAATACCAAATCTCTCAACCAGAAGTGTACGTGGCT 429 GTCACCATGGCAACCTTGTCCCTGGCCCGGCCCTCCTTCAGTTTAGTTGAGGATACCACA 120 CACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTC GACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAGTGGATCAAG GACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGGCCCCACATCCAGTGGATCAAG 1149 CCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGA CCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGA 1089 GTGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGATCG GTGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGATCG 1029 CACTGCAGCCTCATTATGGAAAGTGTGGTCCCATCTGAGAAGGGAAATTATACCTGTGTG CACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTATACCTGTGTG AAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAG 660 AAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAG 909 AACACTGTCAAGTTTGGCTGGCCAGCCGGGGGGAACCCAATGCCAACCATGCGGTGGCTG 600 AACACTGTCAAGTTTCGCTGCCCAGCCGGGGGGAACCCAATGCCAACCATGCGGTGGCTG 849 GCACCATACTGGACCAACACAGAAAAAGATGGAAAAGCGGCTCCATGCTGTGCCTGCGGGCC 540 GTAGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCATCCGGAGAT 669 Similarity Conservative 51.3%; ; Score 2188; DI ; Pred. No. 0; 0; Mismatches DB 12; Length 2676; 60; 0 other; Indels 15; Gaps 360 240 1209 840 780 720 900 N В 1975 GATATUAACAATATACACTATTACAAAAAGACCAATGGGCGGCTTCCAGTCAAGTGG

2034	GATATCAACAATATACACTATTACAAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGG	1975	Db
2280	NTCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTG	22	γQ
1974	CGCCAG	1915	ДĎ
2220	GAAATGTTTTGGTAACAGAAAAACAATGTGATGAAAATAGCAGAG	16	Qy
1914	TIGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCC	æ	Db
2160	GGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGC	$\tilde{\mu}$	Ş
1854	ATTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAG	1795	Db
2100	AACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACC	0	Qy
1794	GCCAACCTCCGAGAATACCTCCGAGCCCGGGAGGCCACCCGGGATGGAGTACTCCTATGAC	1735	Оb
2040	CAACCTCCGAGAATACCTCCGAGCCCGGGAGGCCACCCGGGATGGAGTACTCCTATC	9	Qy
1734	AGTATGCCTC	1675	Db
1980	TTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTA	9	Qy
1674	GGAAACACAAGAATATCATAAA	o,	Db
1920	CTGGTGTCAGAGATGGAGATGAATGAATGATTGGC	1861	Qy
1614	CCACAGAGAAAGACCTTTC	1555	DЬ
1860	AGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATG	1801	νQ
1554	GCTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCCAAG	1495	ДD
1800	GTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCCAA	7	Оу
1494	GAGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCCTGGGAGAA	1435	фd
1740	AGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGG	1681	Q
1434	CGCCTCTCTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCA	1375	DЬ
1680	GCCTCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCC	1621	Qy
1374	GTTTCGGCTGAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA	1315	Db
1620	TTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA	1561	Qy
1314	AGCAGCCAGCCGGCTGTGCACAAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAACA	1255	Db
1560	CAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAACA	1501	γQ
1254	TGTATGGTGGTAACAGTCATCCTGTGGCGAATGAAGAACACGACCAAGAAGCCAGACTTC	1195	Db
1500	TATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACCT	1441	Qy
1194	ACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCC	1135	Db
1440	CAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCC	1381	δ
1134	AGAAAAGGAGATT	1075	ДĎ
1380	TCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATT	1330	Qy
1074	ACCGAGGCGGATGCGGGGAATATATATGTAAGGTCTCCAATTATATAGGGCAGGCCAAC	1015	DЬ
1329	CTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGGATATCCTTT	1270	φ
1014	AAGCACTCGGGGATAAATAGTTCCAATGCAGAAGTGCTGGCTCTGTTCAATGTG	961	DЬ
1269	GCCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATG	10	VΩ
960	CACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTC	901	DЬ

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RESULT 8
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 A cunA library prepared from human cancer cell line Kato III mRNA was screened with an olsopucleotide corresponding to amino acids 529-541 of chicken basic FGF receptor. Three positive clones were obtained one was cloned into pUCIB/19 to give pTB128. The sequence of pTB1229 was the longest of the three clones. See AAQ14848 for pTB1229 winch lacks nucleotides 134-478 and 1399-1314 of pTB1229 and has an A residue in stead of a T at the position corresponding to nucleotide 1029 of pTB1229.
                                                                                                                                                                                                                                                      28-DEC-1990;
27-APR-1990;
31-JUL-1990;
14-SEP-1990;
                                                                                                                           New mutein(s) of proteins - with fibroblast growth factor receptor activity, useful for treating multiple endocrine neoplasia, prostatic hypertrophy, used for diagnosis
                                                                                                        Example 2; Fig 4; 88pp; English.
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                                                  CACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTC
                                                                                                 GACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAGTGGATCAAG
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27-APR-1990;
31-JUL-1990;
14-SEP-1990;
                                                                                           New mutein(s) of proteins - with fibroblast growth factor receptor activity, useful for treating multiple endocrine neoplasia, prostatic hypertrophy, used for diagnosis
                                                                                                                                                                                                                                                                                                                        Clone pTB1283 encoding complete
                                                                                                                          WPI; 1991-353723/48.
P-PSDB; AAR15269.
                                                                                                                                                               (TAKE ) TAKEDA CHEMICAL IND KK
                                                                                                                                                                                                    28-DEC-1990;
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90JP-0113146.
90JP-0204438.
90JP-0245256.
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25..1983
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A cDNA library prepared from human cancer cell line Kato III mRNA was screened with an oligonucleotide corresponding to amino acids 529-541 of chicken basic FGF receptor. Three positive clones were obtained, one was cloned into pUCL18/119 to give pPB1228 (see AAD14848). The complete FGF coding sequence was obtained by lighting the insert from pTB1228 to the DNA sequence of the plasmid pTB1281 insert which enorghes the carboxyl terminus of the FGF receptor from Glu 533 onwards.

Example 3; Fig 8; 88pp; English.

Sequence 2310 BP; 629 A; 566 C; 636 G; 479 T; 0 other;

Query Match

Local Similarity

39.6%;

Score 1689.6; Pred. No. 0;

DB 12; Length

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CGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAG
                           CGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAG 1087
                                                       TGGTGGAGAATGAATACGGGTCCATCAATCACACGTACCACGTGGATGTTGTGGACGAT 1027
TGGTGGAGAATGAATACGGGTCCATCAATCACACGTACCACGTGGATGTTGTGGACGAT 433
                                                                                                                                    AGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTATACCTGTG
                                                                                                                                                                                 TGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACC
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                                                                                                                       AGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTATACCTGTG
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ACATTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACC
                                                                                     ACATTAACCGTGTTCCTGAGGAGCAGGAGGACCTTCAAGGACTTGGTGTCATGCACCTACC
                                                                                                                                                               AAGGCAACCTCCGAGAATACCTCCGAGCCCGGGAGGCCACCCGGGATGGAGTACTCCTATG
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The sequence was obtd. from a clone isolated from a cDNA library

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                Disclosure; Fig
                                    New genetic cloning 
directional cloning
                                                                 WPI; 1991-310282/42.
P-PSDB; AAR14280.
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09-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAACGAACTGTACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAA 2518
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(first entry)
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250..2307
/*tag- b
187..249
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              15; 108pp; English.
                                                                                                                                                                                                                                                            Location/Qualifiers
130. 2310
                                 vectors - which provide efficient, of cDNA copy of a eukaryotic mRNA
                                                                                                                HEALTH
                                                                                                                                                                                                                                                                                                             factor receptor; KGF; tyrosine kinase;
                                                                                            Fleming
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propd. In a new cloning vector, lambda pcPV27. The liberty was propd. from RNA extracted from PARLBAYK syltermal keratinosytes. Property of the part of the part of the part of the part of the period of the property of the part of the part
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Sequence 2345 BP; 621 A; 602 C; 634 G; 488 T; 0 other;

	TCAGCAGCCAGCTGTGCACAAGCTGACCAGGCATCCCCCTGCGGAGACAGGTAA 1129	рь 1070	
	TCAGCAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAA 1558	Qy 1499	0
	CCTGCATGGTGACAGTCATCTTTTGCCGAATGAAGACCACGACCAAGAAGCCAGACT 1069	Db 1010	ы
	CCTGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACT 1498	Оу 1439	0
	TCACGGCTTCCCCAGATTATCTGGAGATAGCTATTTACTGCATAGGGGTCTTCTTAATCG 1009	Db 950	н
	ACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATC	Оу 1379	0
	ACCAGTCTGCCTGGCTCACTGTCCTGCCCAAAGAGCAAGCCCTCTGAGAGAGA	Db 890	ы
		Оу 1328	0
	TGACGGAGATGGATGCTGGGGAATATATATGTTAAGGTCTCCAATTATATAGGGCAGGCCA 889	Db 830	0
	TAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGGATATCCT 1327	Оу 1268	0
	TGAAGCACTCGGGGATAAATAGCTCCAATGCAGAAGTGCTGGCTCTGTTCAATG 829	Db 776	В
	TCAAGGCCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATG 1267	Qy 1208	0
	ACCACGTGGAAAAGAACGGCAGTAAATACGGGCCTGATGGGCTGCCCTACCTCAAGGTCC 775	Db 716	
	AGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTC 1207	Qy 1148	0
	GGGATGTGGAGTTTGCCAAGGTTTACAGCGATGCCCAGCCCCACATCCAGTGGATCA 715	Db 656	ы
	STAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAGTGGATC	0у 1088	0
	CACCACACCGGCCCATCCTCCAAGCTGGACTGCCTGCAAATGCCTCCACGGTGGTCGGAG 655	Db 596	В
	GCCTC	Qy 1028	0
	TGGTGGAGAATGAATACGGGTCCATCAACCACACCTACCACCTCGATGTCGTTGAACGGT 595	Db 536	
	TGGTGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGAT 1027	Оу 968	0
	AGCACTGGAGCCTTATTATGGAAAGTGTGGTCCCGTCAGACAAAGGCAACTACACCTGCC 535	Db 476	ь
	ACCACTGGAGCCTCATTATGGAAAGTGTGGTCCCCATCTGACAAGGGAAATTATACCTGTG 967	Оу 908	0
	TAAAAAACGGGAAGGACTTTAAGCAGGACCATCGCATTGGAGGCTATAAGGTACGAAACC 475	Db 416	В
	TGAAAAACGGGAAGGACTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACC 907	Оу 848	0
	16,	Db 356	0
	CAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGGAACCCAATGCC!	Оу 788	0
	GAGCACCGTACTGGACCAACACAGAAGATGGAGAAGCGGCTCCACGCTGTCCCTGCCC 355	Db 296	D
	GAGCACCATACTGGACCAACACAGAAAAAGATGGAAAAAGCGGCTCCATGCTGTGCCTGCGG 787	Qy 728	0
2;	227; Indels	Best Lo Matches	
	38.5%; Score 1642.8;	65	
	#1100 2340 BF; 621 A; 602 C; 634 G; 466 T; 6 OCHET;	Sequence	Ü

Оу	B 64	Db Oy	рь	рь	D Qy	Db Qy	p Qy	Db Qy	D Oy	D Qy	D Qy	Оy	Оу	Оу	Qу	Оу	Qy Db
2579 2150	2519 2090	2459 2030	2399 1970	2339 1910	2279 1850	2219 1790	2159 1730	2099 1670	2039 1610	1979 1550	1919 1490	8 4	1799 1370	1739 1310	1679 1250	1619 1190	1559 1130
ACTTGGATCTCAGCCAGCCTCTCGAACAGTATTCACCTAGTTACCCTGACACAGAGAGATT 2	COTTCAACCACTIGETAGAAGACTIGGATCGATTCTCACTCTCACACACACACACACACT CCTCTCAACCACTIGGATCACACTCCACACACACACACACTCCACACCAACCACTCGAACTCCCAACCAA	CCAACGAACTGTACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAA 2	TGGAGGAACTTTTTAAGCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCC	TOGGGGTGTTANTGTGGGAANTGTTACTTTAGGGGGTGACCCTACCCAGGANTCCCG 11411111111111111111111111111111111	GGATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGATGTCTGGTCCT 2	GAGRANTEANCAITATRACATATTACAANANGACACACOATGGGGGGGTTCCAGTCAGT   A	CCAGAAATGTTTTGGTAACAGAAACAATGTGATGAAATAGCAACTTTGGATGCGC 	AGCTGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTGGCTG	ACATTAACCGTGTTCCTCAGGACCACATGACCTTCAAGGACTTGGTGTGTTCATCACCTACACCTACCCTACACCACTTCAAGGACTTGGTGTCCTCCACCCTACCCTACCCTTCAAGGACTTGGTGTCCTCCACCCTACCCTACCCTACCCTACCCTACACCTTCAAGGACTTGGTGTCCTTCAACCCTACCCTACCCTACCCTACACCTACACCTACACCTACACCAC	AAGGCAACCTCCGAGAATACCTCCGAGCCCGGAGGCACCCGGGATGCAGTTCGATTTT 2 AAGGCAACCTCCGGGAATACCTCCGAGCCCGGAGGCCACCTGGCATGGAGTACTCCTATG 1 AAGGCAACCTCCGGGAATACCTCCGAGCCCGGAGGCCACCTGGCATGGAGTACTCCTATG 1	ACCTCTGGAGCCTGCACAACAAGATGGCCTCTCTATGTCATAGTTAGGTATGCCTCTATAGTTAGGTATGCCTCTATAGTTAGAGTATGCATGAAATATGCATGAAATATGCATGAAATATGCATGAAATATGCATGAAATATGCATGAATAGTGAAATATGCATGAATAGTGAAATATGCATGAATAGTGAAATATGCATGAATAGTGAAATATGCATGA	GTSATGTGGTGTCAGAAGATGGAGATGATGAAGATGATTGGGAAAGAAA	AGGAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAGACCTTT 1	AGGYTGCTYTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGGAAAGAACAAGCAGCGAAAAAAAA	AGATAAGCTGACACTGGGCAAGCCCCTGGGAG 1 	CACCCTTCTTCAACGCCAAAACCCCCCATGCTGCCAGGGGTCTCCCAGGTMTCAACTTC    1	CAGTTTCGGCCGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCCTGGTGAGGATAACAA 1
638 209	578 149	518	458 029	969	909	278 849	218 789	158 729	969	038 609	978 549	918 489	858 429	798 369	738 309	678	

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                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                             The ectl sequence encoding the KGF receptor was obtd. from a clone isolated from a BALB/MK epidemal kerathocyte DNA library prepd. using the lambda pCEV37 cloning sysem of the invention. The protein appears to typical transmembranc tyrosine tyroses (see AAR10333 for details). closely related to the mouse bfGF receptor.
                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Efficient genetic cloning system - useful for cloning cDNA copies of eukaryotic mRNAs of all sizes and for library preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 15a; 103pp; English.
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                                                                                        A cDNA clone, useful for producing recombinant protein - or
DNA sequence coding Notophthalmus viridscens (newt) acidic
fibroblast growth factor (aFCF)
                                                                                                                                           Chiu IM,
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                                                                                                                                                                                                                                                                                               Notophthalmus viridescens
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This cDNA clone comprises the nucleotide sequence encoding the fibroblast govern fattor receptor 2 (FGFR-2) isolated from the regenerating focelamb blastems of an adult Morophthainus viridacens (newt). It is part of the multigame family of FGFR involved in the The CNA condition of fibroblast growth factors (FGF) a cudic-FGF (BFGF). The CNA clone is used for producing recombinant newt aFGF, which can be used to promote growth of cultured call lines, 9, call lines used to promote growth of cultured call lines, 9, call lines used to promote growth of cultured call lines, 9, call lines are Sequence 2675 BP; 684 A; 716 C; 705 G; 570 T; 0 other; to produce other recombinant proteins, or to promote wound

Disclosure; Columns 27-32; 44pp; English

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                                Query Match
Best Local Similarity
Matches 1654; Conserv
648 AGATGCCATCTCATCCGGAGATGATGATGATGATGACACCGATGGTGCGGAAGATTTTGTCAG 707
                                 Conservative
                                           32.08;
                                 0
                                            Pred. No.
                                                        Score 1367.6;
                                 Mismatches 429; Indels
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                               GTACTCCTTTGACATCAACAGAATTCCTGAAGAGCAGATGACCTTCAAGGACCTAGTGTC
                                                   GTACTCCTATGACATTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTC
                                                                                          AAATATCATCAATCTTCTAGGAGCGTGCACCCAAGATGGCCCACTCTACGTGATAGTCGA 1742
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Qy 26		Qy 25 Db 23	Qy 25 рь 25	Оу 24 рь 23	Qy 2:	Qy 2:	Qy 2; Db 20	Qy 2;	Qy 21 Db 15	рь 18
2688 2463	2628 2403	2568 2343	2508 2283	2448 2223	2388 2163	2328 2103	2268 2043	2208 1983	2148 1923	63
CGAACCATGCCTTCCTCAGTATCCACACATAAACGGCAGTGTTAAAACATGA 2739	CARAGAGITETGTTCTTCTGGGGATGATTCTGTTTTTTCTCCGGACCCCATGCCTTA	CANTGAGGANTACTTGGACCTCAGCACCTCTGGAGCAGGTATTGACCTAGTTAGCCGA 	COGACACCACCETTCAACCACTTGCTACAACACTTGGTCGATCCACTTCACCCCCCCC	AGCCAACTGCACCAACGAACTGTACATGATGATGAGGACTGTTGGCATGCAGTGCCCTC 2	AGGATTCCCGTGGAGGAACTTTTTAAGCTGCTGAAGGAAG	TOTOTOGOTOCTICOGGGGTTTMANGGTGGGAGATCTTCACTTTMAGGGGGGTCCCCCTACCCCCCCCCC	TCCAGTCAAGTGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGA	TGANTGCCAGGARATCANCANATARANTHINGAAAAGACACCAATGGGGGGGT 	AGATTPACCACCAGAAATGTTTTTGTTAACGAAAACAATGTGATGAAAATAACAACTT 	
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AAX85614 standard; cDNA; 2675 ВP

# AAX85614;

06-SEP-1999 (first entry)

# Bek-like newt FGFR2 cDNA

Acidic fibroblast growth factor: aFGF; wound healing; tissue repair; non-acidic fibroblast growth factor; nitogaic response; Tr31-5-1; Tr33-1-2; truncated form; newt; receptor; ds.

### Notophthalmus viridescens

30-JUL-1997; 97US-0885418.

20-JUL-1999

28-MAY-1993; 30-JUN-1997; 93US-0070165. 97US-0885418.

(OHIS ) UNIV OHIO STATE RES FOUND

Chiu IM

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Disclosure; Columns 27-32; 44pp; English. non-acidic fibroblast growth factor proteins Distinguishing between the biological activities of acidic and P-PSDB; AAY23631. WPI; 1999-418269/35

SXCCCCCCCCCCCCCXXXTTXRR (non-refer) proteins. For proteins are thought to be involved in wound healing and tissue repair. The method comparies determining and comparing the mitogenic responses of Tr31-5-1 (ATCC CRL-1521) and Tr31-1-2 (ATCC CRL-1521) and Tr31-1-2 (ATCC CRL-1521) call lines to different forms of aFCF and non-aFCF proteins. The method may be used for different tening bloogical activities among the full length form and truncated forms of aFCF proteins and other (non-aFCF) proteins. The intermethod forms of aFCF proteins and other (non-aFCF) proteins. The intermethod forms of aFCF may be used to better unders by the molecular basis of the mouthfloss. The same of aFCF are trivity in a condition of aFCF are trivity in the basis for the are triving in deal conditions. This understanding provides the basis for the are triving leasing to both lighted and AFCF are triving against a grant and after protein a grant and are triving against a grant and are triving a dealing of both lighted and AFCF are triving against a grant and are triving a dealing of the present are triving and are triving against a grant and are triving a dealing of the present are triving and are The specification describes a method for differentiating biological socilytiles among the full length form of scidic fibroblast growth factor (aFGF) proteins and other non-acidic fibroblast growth factor sequence encodes bek-like newt fibroblast growth factor receptor FGFR2

Sequence 2675 BP; 684 A; 716 C; 705 G; 570 T; 0 other;

Query Match Best Local 9

Similarity

32.0%; 79.1%;

DB 20; Length 2675;

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õ á ş В 5 밁 Š 밁 δÃ В S 망 DЬ Ъ Matches 1654; 1008 789 729 948 669 888 609 828 549 768 492 708 432 648 AGATGCCATCTCATCCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAG 7,07 CCTGGATGTTGTGGAGCGATCGCCTCACCGGCCATCCTCCAAGCCGGACTGCCGGCAAA 1067 TACGCCCTCCATGAGGTGGCTGAAGAACGGCAAGGAGTTCAAGCAGGAGCACCGCATTGG GCTCCATGCTGTGCCTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGAACCCC 827 CCTGGATGTTGTCGAGCGGTCACCCCACCGGCCAATACTCCAAGCTGGGCTTCCGGCAAA 848 CGGCTTCAAGGTAGTCAACACTTCAGCCTGATCATGGAGAGCGTGGTTCCCTCTGA 728 AGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGA 947 AATGCCAACCATGCGGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGG 887 TGACAAC---AACCACATGAGGGCTCCGTACTGGACGAATACAGAAAAATTGGAAAAGAA 548 TGAGAACAGTAACAACAAGAGAGCACCATACTGGACCAACACAGAAAAGATGGAAAAGCG 767 AGATGCAAACTCATCAGGGGATGATGAAGACGACGACGACGGCTCGGAAGATTTCACAAA 491 ACTCCATGCTGTGCCGCTGCCAACACTGTGAAGTTCCGCTGTCCAGCCGGTGGCAACCC 608 Conservative Score 1367.6; DB 20 Pred. No. 0; 0; Mismatches 429; Indels 9 Gaps

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1248 GGTTCTCTATATTCGGAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGG 1307

GCATCCCTATCTGAAAGTGCTAAAGGCGGCCGGTGTTAACACCACGGACAAAGAGATCGA GCTGCCCTACCTCAAGGTTCTCAAGGCCGCCGGTGTTAACACCACGGACAAAGAGATTGA 1247 GCCACATATCCAATGGATTCGACATTTTGAGCTGAATGGCAGTAAAATTGGACCTGACGG

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AGTCCTCTATGTGGGGATGTCTTTTTGAGGATGCTGGGGAGTATACGTGCTTGGCGGG

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1068 TGCCTCCACAGTGGTCGGAGGGGAGACGTAGAGTTTGTCTGCAAGGGTTTACAGTGATGCCCA 1127

849 CACAACCACAAAAGTTGGGGGCGATGCAGAGTTTGTTTGCAAAGTCTACAGTGACGCACA 908

GCCCCACATCCAGTGGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCCGACGG 1187

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2328 TGTCTGGTCCTTCGGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTACCC 2387	Db Q
2268 TCCACTCAACTGAATGGATGGCTCCAGAACCCTGTTTGATAAGAGTATACAGTATACAGATGAA 2327 2043 CCCCGTGAAGTGGATGGCTTCCCGAGGGCCTGTTTGACAGAGTCTACACACATCAGAGTGA 2102	Db
2208 TGGACTCGCCAGAGATATCAACAATATAGACTATTACAAAAAAGACCACCAATGGGCGGCT 2267 	рь
2148 AGATTPACCAGCAAAATGTTTTGGTAACAGAAAACAATGTGTGATGAAAAACAATGCAGCAGCTT	Db Oy
2088 ATCACCTACCACCTGGCCAAGGCATGGAGTACTTGGCTTGCCAAAAATTATTCATCG 247	D 04
2028 GTACTCCTATGACATTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTC 2087	Оy
1968 GTATROCTYCTAAGGCAACCTYCGAGAANAACTYCGGGGCGGGGGGGGGGGGGGGGGGAGGGAGGGAGGGAGG	рь
1998   GAPTAPCAPAARCTPCTAGGAGCTCCAACAGARGGGCCCTCTCTGCCCAPACTTCA   1967   1968   1967   1968   1967   1968	Db Oy
1848 GAAAGACCTTTCTGATCTGGTCTCAGAGATGGAGATGATGAAGATGATGAGAACAACAA 1907 	Db 09
1788 ABACANGGCANGGAGGGGGCACCGTGGAGATTTTGANAGGTGATGCGACAGA 1847 1789 ABACANGCCANAGATGCACGACGTGAGGATGGAAGATTTTGANAGGAGATGCAACGA 1622 1563 GGACGGGCCCANAGATGCAGGACGGTGGAGGTGGAAGATGCTGANAGAGATGCAACGA 1622	DP QA
1728 GCCCCTGGGAGAAGGTYBCCTTTGGGCAAATGGTCAATGGCGGAAGAGTGGGAATTGAAATTAAAA 1787   1111   111   1	Db Qy
1668 GTATGAACTTCCAGAGGACCCAAAATGGGAGTTTCCAAGGAATAAGCTGACACTGGGCAA 127 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Db 03
1608 GAGGATAACAACACCCTCTCTTTAACGGCAGAACACCCCCATGCTGGGAGGGTCTCCGA 1667	Оβ
1548 GAGACAGGTAACAGTTTCGGCTGACTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGT 1607 	Оу
1488 GAAGCAGACTTCAGGAGCGGCGCTGTGGACAAGCTGACAAAGCTGCCCCTGCG 1547	Db Qy
1428 CTTCTTAATGGCCTGTATGGTGGTAAGAGTCATCCTGTGGCGAATGAAGAACAGGACCA 1487	Оy
1368 AGAAAGGAGATTACAGCTTCCCAGACTACCTGGAGATAGCCATTTACTCCATAGGGT 1427	Оγ
1308 TAATTCTATTGGGATATCCTTTCACTCTGGATGGTTGACAGTTCTGCCAGGGGCTGGAAG 1367	Оy

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RESULT 14
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27-APR-1990;
31-JUL-1990;
14-SEP-1990;
was screened with an oligonuclectide corresponding to amino acids 529-541 of chicken basic PGF receptor. Three positive clones were obtained. One was cloned into pUC118/119 to give pTB1228. The sequence of pTB1228 is shorter than that of pTB129 lacking nucleotides 134-478 and 1309-1314 (see AAQ14849).
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                                                          A cDNA library prepared from human cancer cell line Kato III mRNA
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                                                                                                       muteln(s) of proteins - with fibroblast growth factor
eptor activity, useful for treating multiple endocrine
plasia, prostatic hypertrophy, used for diagnosis
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                                                                                   2; Fig 3; 88pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding protein with FGF receptor activity
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90JP-0113146.
90JP-0204438.
90JP-0245256.
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CAGAGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAG
                                               CACGCCTCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGGAGTATGAACTTC
                                                                                                               CAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAA 1618
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                               CACGCCTCTCTTCAACGGCAGACACCCCCCATGCTGGCAGGGGGTCTCCGAGTATGAACTTC
                                                                                                                                                             TCAGCAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAG----
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                                       28-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                    recombinant protein; fibroblast growth factor; FGF
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Best Local
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           TAATTCTATTGGGATATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAG
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                                                                                                                                                                                                                                                                                       CCTGGATGTTGTGGAGCGATCGCCTCACCGGCCCATCCTCCAAGCCGGAACTGCCGGCAAA 1067
                                                                                                                                                                                                                                                                                                                             CGGCTTCAAGGTACGTAGTCAACACTTCAGCCTGATCATGGAGAGGGGTGGTTCCCTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                      AGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGA 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTCCATGCTGTGCCCGCTGCCAACACTGTGAAGTTCCGCTGTCCAGCCGGTGGCAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCCATGCTGTGCGGCCAACACTGTGTCAAGTTTCGCTGCCCAGCCGGGGGGAACCC
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                                                               GGTTCTCTATATTCGGAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGG 1307
                                                                                                                                                                                    GCCCCACATCCAGTGGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGG 1187
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                                                                                                 GCATCCCTATCTGAAAGTGCTAAAGCGCTCTGGAATTAATAGCTC-----CAATGCCGA
                                                                                                                          GCTGCCCTACCTCAAGGTTCTCAAGGCCGCCGGTGTTAACACCACGGACAAAGAGATTGA 1247
                                                                                                                                                          GCCACATATCCAATGGATTCGACATTTTGAGCTGAATGGCAGTAAAATTGGACCTGACGG
                                       AGTTCTGACCCTGCATAACGTGACTGAGGCGGACCGGGGCCAGTACACATGCAAAGTCTC
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This cDNA clone comprises the nucleotide sequence encoding the Keratinodyle growth factor receptor (KGPR) isoform isolated from the regenerating forelimb blastems of an adult Motophthalmus viridscens (newt). It is fibroblast growth factor (FGF) related with properties of a paracine effector of epithelial cell growth. The properties of a paracine effector of epithelial cell growth can be used for producing recombinant new aFGF, which can be used to promote growth of cultured cell lines, e.g. cell lines used to produce other recombinant proteins, or to promote wound best of the produce other recombinant proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A cDNA clone, useful for producing recombinant protein - comprises 
DNA sequence coding Notophthalmus viridscens (newt) acidic fibroblast growth factor (aFGF)
648 AGATGCCATCTCATCCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAG
                                                                                      Score 1276.4; DB 19
Pred. No. 2.9e-305;
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2441	2382 CTACCCAGGGATTCCCGTGGAGGAACTTTTTAAGCTGCTGAAGGAAG	
2381 2162	2322 GAGTGANGTCTGGCCTTGGGGGTGTTAATGTGGGAGATCTTTCACTTTAGGGGGCTCGCC 2103 GAGTGACGTCTGGCCTTTCGGTGTTAATGTGGGAGATCTTCACACTGGGGTTCCCC 2103 GAGTGACGTCTGGCTTTTCGGTGTTATGTGGGAGATTCCCC	
2321 2102	2252 GCGGCTTGCAGTGAGTGGATGGCTGCAGAAGGCCCTGTTTGATAGAGTATACACTGATCA	
2261 2042	2202 AGACTITIGGACICGCCAGAGATATCAGCAATATAGACTATTAGCAAAAAAGACCACCAATGG	
2201 1982	2142 TCATCGAGATTHAGCACCCAGAAATGTTTTGGTAACAGAAACAATGTGATGAAAAAAGAG 1911   1   1   1   1   1   1   1   1   1	
2141 1922	2082 GGTGTCATGCACCTACCAGCTGGCCAGGCATGGAATGGA	
2081 1862	2022 GATGGAGTACTCCTATGACATTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTT	
2021 1802	1952 AGTIGAGTATGCCTCTAAAGGCAACCTCCGAGAATACCTCCGAGCCCGGAGGCACCCGG	
1961 1742	902 ACACAAGAATATCATAAATCTTCTTGGAGCCTGCACACGAGGATGGGCCTCTCTATGTCAT 	
1901 1682	842 CACAGAGAAGACCTTTCTGATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGAA	щ ц
1841 1622	1782 TRANSAGREAGCCCAAGGGGGGTCACCGTGGCCCGTGAAGATGTTGAAAGATGCTGATGC	<b>,</b> ,
1781 1562	722 GGCCAAGCCCTGGGAGAAGGTTGCTTTCGGCAAGTGGTCATGCGGAAACAGTGGGAAT 101   11   11   11   11   11   11   11	
1721 1502	662 CTCCCAGATROANCTTCCNGAGGACCXAAATGGGACTTTCCNAGAGATAACGAGAACT 	
1661 1442	602 GCTGGTGAGGATAACAACACGCTCTCTTCAACGGCAGAGACACCCCCATGCTGGCAGGGTT	
1601 1382	542 CCTGCGGAGACAGGTAACAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCC	щ ц
1541 1322	482 GACCAAGAAGCCAGACTTCACCACCCAGCCGGCGGTGTGCACAAGCTGACCACAACCTARTCCC	
1481 1262	422 AGGGTCTTCTTAATCGCCTGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACAC 	ب ب
1421 1202	368AGAAAAGGAGATTACAGCTTGCCCAGACTACCTGGAGATAGCCATTTACTGCAT	
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2622 CCCTGACACAGAGGTCTTGCTGCTGCTGCTGCTGTGTTTTTTCTCCAGACCCCAT 2681
2610 TCCGGGATACCAGGAGTTCCTGCTCTTCTGGGGATGACTCTGTCTTCTCCCCGGACGCAAT 2462
                                                                                                                   252 CACAACCAATAGGAATACTTGGACCTCAGCAACCCTCTGGAACAGTATTGACCTAGTTA 2621
2343 AACGACCAATGAGGAATACTTGGACCTCCTAGAACAACCCTCTGGAGCAGTACTCGCAGCTA 2402
                                                                                                                                                                                                                                       2502 GCCCTCCCAGAGGCAACGTTCAAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCT 2561
                                                                                                                                                                               2283 GCCCTCGCAAAGACCCACTTTCAAGCAGCTTGTTGAGGATCTAGACCGAATCCTCACGCA 2342
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Copyright (c) 1993 - 2002 Compugen Ltd
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12	1182.2		2469	-	-459	,-	
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14		27.7	2662	N	US-08-451-822A-14	14	
15			2662	4	US-08-323-430-14	14,	
16			2733	_	US-08-371-001-14		
17	1159.2		2733	v	PCT-US96-00331-14	14	
18	1141	26.7	3503	_	US-07-631-717A-1	,	
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20	981.8	23.0	5993	4	-09-383-	Sequence 1, Appli	
21	981.8		5993	4	-630-	N	
22	961.8	22.5	2049	4	US-09-099-749-10	10	
23	956.2		8083	4	630-		
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25	931.6		1079	H	-08-471	Ξ.	
26	623.2	14.6	1875	_	-08-070-165F-		
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192.8	192.8	192.8	192.8	192.8	192.8	194	197.4	205	205	245.4	426.2	542.2	597.6	598.8	603.4	623	623
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5406	5406	5406	5406	5406	5406	3845	360	4138	4138	4508	1983	734	933	1056	605	1839	1839
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US-08-601-891-5	US-07-906-397A-5	US-08-252-517-5	US-07-946-507-3	US-07-977-451-5	US-07-813-593-3	US-08-220-240A-4	PCT-US93-05703-1	PCT-US93-06093-1	US-08-323-474-1	PCT-US93-06251-34	US-09-057-860A-8	US-08-471-570-11	US-08-701-191A-4	US-08-701-191A-5	US-08-471-570-1	US-08-885-418-7	US-08-070-165F-7
Sequence 5, Appli	5	ū	ü	S	ω	4	-	<u>,</u>	,	Sequence 34, Appl	80	Sequence 11, Appl	4	ū	<u>,</u>	7	Sequence 7, Appli

## ALIGNMENTS

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US-08-451-822A-15
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Patent No. 586388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM. PC DOS/MS-DOS
SOTTWARE: PatentIN Release #1.0, \
CURRENT APPLICATION NUMBER: 195/08/451,822/
                                                                                                TELEFAX: (610) 454-3808 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                FILING DATE: 26-MAY-1955
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,430
FILING DATE: 14-0CT-1994
PRIOR APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-AUG-1992
PRIOR APPLICATION NUMBER: US 07/549,587
APPLICATION NUMBER: US 07/549,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dionne
                                                                                                                                                                                          APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: SAVIERRY, MARTIN
REGISTRATION NUMBER: 39,999
REFERENCE/DOCKET NUMBER: A0496E
                                                                                                                                                           TELEPHONE: (610) 454-3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Crumley, Greg
APPLICANT: Jaye, Michael C
APPLICANT: Schlessinger, Joseph
TITLE OF INENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Legal Department
TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 500 Arcola
CITY: Collegeville
STATE: PA
                                       STRANDEDNESS:
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δ 5 ð Ş Ş Вb õ 문 Ş В ş В Ş В á 밁 Ş B οy 멍 8 밁 Š 망 õ В Ş р Ş Ş 망 В g В US-08-451-822A-15 Matches 3411; Query Match 1053 CGGACTECCGGACAATGCCTCCACATGGTCGGAGGAGAGCTTAGACTTGTCTGCAAGGT 1112
960 CGGACTECCGGCAAATGCCTCCACAGTGGTCGGAGGAGAGCGTAGAGTTTGTCTGCAAGGT 1019 900 993 873 660 600 693 540 633 480 573 420 513 360 453 300 393 240 333 180 273 120 213 933 720 813 753 153 780 19 Local Similarity 93 CACAGGTCGCGGAGGAGCGTTGCCATTCAAGTGACTGCAGCAGCAGCGGCAGCGCCTCGG 152 TTCCTGAGCCCACCGCAGCTGAAGGCATTGCCGCTAGTCCATGCCCGTAGAGGAAGTGT 212
TTCCTGAGCCCACCGCA-GCTGAAGGCATTGCCGCGTAGTCCATGCCCCGTAGAGGAAGTGT 119
TTCCTGAGCCCCACCGCA-GCTGAAGGCATTGCCCGTAGTCCATGCCCGTAGAGGAAGTGT 119 CATGGTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGGATGACACCGATGGTGC 692 CAAATACCAAATCTCTCAACCAGAAGTGTACGTGGGCTGCGCCAGGGGAGTCGCTAGAGGT 452 GCCCGGCCCTCCTTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAAGAGCCCACCAAC 392 CATGGTCAGCTGGGTCGTTTCATCTGCCTGGTCGTCACCATGGCAACCTTGTCCCT CATGGTCAGCTGGGGTCGTTTCATCTGCCTGGTCGTCGTCACCATGGCAACCTTGTCCCT 332 GCAGATGGGATTAACGTCCACATGGAGATATGGAAGAGGACCGGGGATTGGTACCGTAAC 272 CAATCACACGTACCACCTGGATGTTGTGGAGCGATCGCCTCACCGGCCCATCCTCCAAGC 959 CAATCACACGTACCACCTGGATGTTGTGGAGCGATCGCCTCACCGGGCCCATCCTCCAAGC 1052 GGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTATGGAAAG 932 AGCCGGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAGGAGTTTAAGCA 872 CATGGTGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGGATGACACCGATGGTGC AGACTCCGGCCTCTATGCTTGTACTGCCAĞTAGGACTGTAGACAGTGAAACTTGGTACTT 632 GCCCAACAATAGGACAGTGCTTATTGGGGAGTACTTGCAGATAAAGGGCGCCACGCCTAG GCCCAACAATAGGACAGTGCTTATTGGGGAGTACTTGCAGATAAAGGGCGCCCACGCCTAG CAAATACCAAATCTCTCAACCAGAAGTGTACGTGGCTGCACCAGGGGAGTCGCTAGAGGT GGCCCGGCCCTCCTTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAAGAGCCACCAAC GCAGATGGGATTAACGTCCACATGGAGATATGGAAGAGGACCGGGGGATTGGTACCGTAAC GGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTATGGAAAG AAAGATGGAAAAGCGGCTCCATGCTGTGCCTGCGGCCAACACTGTCAAGTTTCGCTGCCC 812 AGACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAGACAGTGAAACTTGGTACTT ACCCGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGGAAGGAGTTTAAGCA Conservative 79.3%; 0 Score 3386.6; Pred. No. 0; Mismatches DB 2; 4; Indels Length 3416; 2 Gaps 839 779 539 572 299 239 179 599 479

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GAGCAGATGCCTT GGACCAGATGCCTT GGACTTGCCA GTACTTGGCTTCCCA GTACTTGGCTTCCCA GTACTTGGCTTCCCA AGAAAACAATGTGAT AIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		TOGGGAGTTTCCAAGAGATAA  TOGGAGTTTCCAAGAGATAA  TOGGAGTTTCCAAGAGATAA  CAAGTGGTCATGGCGGAAGC  LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CATCCTGTGCGAAT	MANGANGGGCAGTAA
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CACATAATTTCTTAATTTTCACCGAGCAGAGGTGGAAAAATACTTTTGCTTTCAGGGAAA
                               AATGCACCTAGAAAATTGGTCTCTCTTTTTTAATAGCTATTTGCTAAATGCTGTTCTTA 327:
                                                                        AAATATATATATATATTACAAGGAGTTATTTTTTGTATTGATTTAAATGGATGTCCC 3212
                                                                                                                  CAGAATGGATAAGCCAGCCAACTGCACCAACGAACTGTACATGATGATGATGAGGGACTGTTG
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                                                              AAATATATATATATATTTACAAGGAGTTATTTTTTTTTGTATTGATTTTAAATGGATGTCCC
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Conservative

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Mismatches

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2 Gaps

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Local Similarity

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                                                  ; MOLECULE TYPE:
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US-08-323-430-15
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  Query Match
Best Local
                                                                                                                               TELEPHONE: (215) 454-38:
TELEPAX: (215) 454-3808
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc R
STREET: 500 Accola Road
CITY: GOLDGEVILLE
COUNTE: PALOGEVILLE
COUNTE: USA
ZIP: 19425
                                                                                                                                                                                                               APPLICATION NUMBER: US 07/549,587
ETLING DATE: 06-ULT-1990
ATTORNETY AGENT INFORMATION:
NAME: GOODMan, Resannes
REGISTRATION NUMBER: 32,534
REFERENCE/MOKET NUMBER: A0496
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dionne, Craig A
APPLICANT: Crumley, Greg
APPLICANT: Jaye, Michael C
APPLICANT: Jaye, Michael C
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibroblast (
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3360
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                                                                                   TOPOLOGY:
                                                                                                 TYPE: nucleionstrandedness:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US to FILING DATE: 21-AUG-1992 APPLICATION NUMBER: US 0 FILING DATE: 06-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGTATAACGTTAATTTATTAATAAATTGGTAATATACAAAACAATTAATCATTTATAG 3392
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                                                                                                                 nucleic acid
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79.3%;
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Score 3386.6;
Pred. No. 0;
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                DB
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1292	GGACAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACTTTTGAGGACGCTGGGGAATA	1233	9
1232 1139	ATACGGCCCGACGGCTTGCCCTACCTCAAGCTTCAAGGCCGCGCGGTGTTAACACCAC	1173	Db 99
1172 1079	TTACAGTGATGCCCAGCCCCACATCCAGTGGATCAAGCACGTGGAAAAGAACGGCAGTAA 	1113	p 94
1112 1019	GGACTGCCGGCAAATGCCTCCACAGTGGTCGGACGAAACGTAGAGTTTGTCTGCAAGGT	1053 960	g 9
959	CAATCACACGTACACCTGGATGTTGTGGAGGATGGCCTCACCGGCCGATCCTCCAAGC	900	B 4
99	TGTGGTCCCATCTGACAAGGGAATTATACCTGTGTGGGAGAATGAAT		8
992	TGTGGTCCCATCTGACAAGGGAAATTATACCTGTGTGGTGGAGAATGAAT	933	Qy
w	- GGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTAT	80	В .
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872	AGCCGGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAGGAGTTTAAGCA 	913 720	B 8
719	AAAGATGGAAAAGCGGCTCCATGCTGTGCCTGCGGCCAACACTGTCAAGTTTCGCTGCC	o,	. B
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752	GAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGAGCACCATACTGGACCAACACAG	693	δ
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419	GCGCTGCCTGTTGAAAGATGCCGCCGTGATCAGTTGGACTAAGGATGGGGTGCACTTGG	360	Db
512	GCCCTGCTGTTGAAAGATGCCGCCGTGATCAGTTGGACTAAGGATGGGGTGCA	453	Q
	-	300	Dβ
452	AAATACCAAATCTCTCAACCAGAAGTGTACGTGGCTGCGCCAGGGGGAGTCGCTAGAGG	393	γo
299	GCCCGGCCCTCCTTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAAGAGCCACCAAC	240	В
392	GCCCGGCCTCCTTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAAGAGCCACCAA	333	Qy
ω e	CATGGTCA	æ	Db .
	CATRRETCARCITORACITATE ATTRETCATOR TOTAL ATTRETCATOR A	7	Ş
179	CARATIGGATTAAGGTCCACATIGGAGATATIGGAGGAGGAGGGGGATTGGTACGTTAAG 	120	용 5
	TTCCTGAGCCCACCGCA-GCTGAAGGCATTGCGCGTAGTCCATGCCCGTAGAGGAAGTG	- 5	В

2372 2279	CACTCATCAGAGTGATGCTGGTCCTTCGGGGGTTAATGTGGGAAATCTTCACTTTAGG	2313	Оy
21		16	Дb
2312	ACCAATGGGCGGCTTCCAGTCAAGTGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATA	2253	γQ
2252 2159	GAAAATAGCAGACTTTGGACTCGCCAGAGATATCAACAATATAGACTATTACAAAAAGAC  [ 1	2193 2100	Qy db
2099	STATTCATCGAGATTTAGCAGCCAGAAATGTTTTGGTAACAGAAAACAATGTGAT	04	Db
2192	AAAATGTATTCATCGAGATTTAGCAGCCAGAAATGTTTTGGTAACAGAAAACAATGTGAT	2133	Qy
3		98	Db 42
٠ س	あるつつ あつ サイフ・ボーク はっしゅうしゅう こうじゅう こうじゅう かんりゅう かいしゅう かんしゅう アンドラス・アンド	3	2
2072	CCACCCGGGATGGAGTACTCCTATIGACATTAACCGTGTTCCTGAGGAGCAGATGACCTT	2013 1920	о <sub>у</sub>
1919	ATGTCATAGTTGAGTATGCCTCTAAAGGCAACCTCCGAGAATACCTCCGAGCCCGGAG	00	Db
2012	CTATGTCATAGTTGAGTATGCCTCTAAAGGCAACCTCCGAGAATACCTCCGAGCCCGGAG	1953	ОУ
1859	GATTGGGAAACACAAGAATATCATAAATCTTCTTGGAGCCTGCACACAGGATGGGCCTCT	1800	DЬ
1952	ATTGGGAAACACAAGAATATCATAAATCTTCTTGGAGCCTGCACACAGGATGGGCCTCT	00	Qy
79		7.4	Db .
æ	atgatgccacagagaaagacctttctgatctggtgtcagagatggagatgatgaagat	1833	40
1739	AGTGGGAATTGACAAAGACAAGCCCAAGGAGGCGGTCACCGTGGCCGTGAAGATGTTGAA	83	DЪ
8	GTGGGAATTGACAAAGACAAGCCCAAGGAGGCGGTCACCGTGGCCGTGAAGATGTTGAA	7	у
67	GCTGACACTGGGCAAGCCCCTGGGAGAAGGTTGCTTTGGGCAAGTGGTCATGGCGGAAGC	62	DЪ
1772	CTGACACTGGGCAAGCCCCTGGGAGAAGGTTGCTTTGGGCAAGTGGTCATGGCGGAAGC	1713	γο
1619	GCAGGGGTCTCCGAGTATGAACTTCCAGAGGACCCAAAATGGGAGTTTCCAAGAGATAA		Db
1712	GCAGGGGTCTCCCGAGTATGAACTTCCAGAGGACCCCAAAATGGGGAGTTTCCCAAGAGATAA	1653	δ
55		0	Db
1652	ACACCCGGCTGGTGAGGATAACAACACGCCTCTCTTCAACGGCAGACACCCCCATGCT	1593	Qγ
49	ACGTATCCCCCTGCGGAGACAGGTAACAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTC	44	DЬ
1592	GTATCCCCCTGCGGAGACAGGTAACAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTC	S	γQ
1439	GAAGAACACGACGAAGAAGCCAGACTTGAGCAGCCAGCCTGTGCACAAGCTGACCAA	1380	рь
1532	AAGAACACGACCAAGAAGCCAGACTTCAGCAGCCAGCCGGCTGTGCACAAGCTGACCAA	1473	γo
37	TTACTGCATAGGGGTCTTCTTAATCGCCTGTATGGTGGTAACAGTCATCCTGTGCCGAAT	32	Db .
47	TACTGCATAGGGGTCTTCTTAATCGCCTGTATGGTGGTAACAGTCATCCTGTGCCGAAT		0
<u>u</u>		26	Db
41	CCAGCGCCTGGAAGAGAAAAGGAGATTACAGCTTCCCCCAGACTACCTGGAGATAGCCAT	ū	γQ
5		20	Db .
1352	ACGTGCTTGGCGGGTAATTCTATTGGGATATCCTTTCACTCTGCATGGTTGACAGTTC	1293	γο
1199	GGACAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACTTTTGAGGACGCTGGGGAATA	1140	DЪ

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                                                                    ATGGTATAACGTTAATTTATTAATAATTGGTAATATACAAAACAATTAATCATTTATAG
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US-08-471-570-7
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GENERAL INFORMATION:
APPLICANT: IGRAESHI, Koichi
APPLICANT: SENCO, Masaharu
APPLICANT: WATANABE, Tatsuya
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 2261; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING DATE: PC-DOS/MS-DOS
OPERATING DATE: PC-DOS/MS-DOS
OPERATION UNUSER: US-08/149.564
PFILING DATE: PC-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/MS-DOS/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200291 STRE UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
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CITY: Boston
STATE: Massac
COUNTRY: US
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STRANDEDNESS: doub
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ADDRESSEE: CUSHMAN
                                                                                                             GTCACCATGGCAACCTTGTCCCTGGCCGGGCCTCCTTCAGTTTAGTTGAGGATACCACA
TTAGAGCCAGAAGAGCCAACCAAATACCAAATCTCTCAACCAGAAGTGTACGTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (617)523-6440
                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 0;
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AGCAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAACA 156	CGACCAAGAAGCCAGACTTC 1 	ACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCC 144 	TGCCAGCGCCTGGAGAGAGAAAGGAGATT 13      	CGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGGATATCCTTT 1 	ACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATGTA 1	CACCTICAAAAAAACGCATATATTC 120 CACCTICAAAAAAAAACGCATATATTC 120 CACCTICAAAAAAAAACGCATATATATATATATATATATATATATA	GACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCAGATCCAGTGGATCAAG 114 	CCTCACCGGCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGA 108 	GTGGAGAATGAATACGGGTCCATGAATCACACGTACCACCTGGATGTTGTGGAGGGATCG 102 	CACTGGAGCCTCATTATGGAAACTGTGGTCCCATCTGACAACGGAAATTATACCTGTGTG 969	ADADACGGAAGACATTTAACCAGGACCATCGCATTGGAGGTACAAGGTAGGAAGCAGGAACAGAGGAAGAGAGAG	AACACTGCAAGTTTCGCTGCCCAGCCGGGGAACCCAATCCAACCATCGGGGGGGTGG 89	CONCENTACTION CONCENTANTALITY   1	GATGAGATGALACGATGGTGGGGAAGATTTGTCAGTGAGACACTACACACAGGAGA 729 	GTAAAASATAAACTIGGTACTTCATGGTGAATGTAAAGAGTGGCATGTCATCGGGAAT 669 	CAGATAAAGGGGGCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACT 609 	ACTANGANTGAGTCACTTGGGGCCAACANTAGAACATCCTTATTGGGAGATACTTG 49 	GCGCCAGGGGAGTCGCTAGAAGTTGCGCTGCTGTTGAAAGATGCCGCCGTGATCAGTTGG 489
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1555 ROCAGCCAGCAGCTOTCCACANAGCTACCANAGTTCCCCCTGGGAACACCTACCACACACACACACACACA	Db	Qy	рb	Qy	DЬ	Qγ	Db	Qy	Db	γQ	рb	νo	рb	γQ	фa	Qγ	Db	Qy	ф	QΥ	рь	γo	рb	Qy	Db	Qy	DЬ	Qy	Вb	Qy	Вb	0y	Dь	Qy	рь
GENECCHOCGGGTGTGCACCAAGCTGCACCAAGCGTATCCCCCTTCCGAGACAACCGTTCCCACCAACCGTGGCACCACCACCGTGGGAGATAACACA 1 TTTCGGCTGAGTCCACCACCCCCATGACTGCACCACCCCCTTCCGAGATAACACA 1 TTTCGGCTGAGTCCACCACCACCCCCATGCTGGGAAGCGGGTTCCGAGTAACACACA 1 GCCTTCTTCAACGGCAACACCCCCCATGCTGGGCAGGGGTTCCGAGTATCAACTTCCA IIIIIIIIIIIIIIIIIIIIIIIIIII	27	52	21	46	15	40	9	34	03	28	97	22	91	16	85	_	79	24	73	98	67	92	61	98	55	0.8	49	74	43	68	37	62	31	56	25
	CANGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCTCACAACCAATGAG 23	CAAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCTCACAACCAATGAG 257	CGAACTGTACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACG	CGAACTGTACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACACCAACG 2	AGGAACTTTTTAAGCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCC	AGGAACTTTTTAAGCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCC	GGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCGTG	GGTGTTAATGTGGGAGATCTTCACTTTAGGGGGGCTCGCCCTACCCAGGGATTCCCGTG 2	TGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTC	TGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTC 2	ATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGG	ATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGG	AAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGACTTTGGACTCGCCAGA	GAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGACTTTGGACTCGCCAGA 2	TGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCC 1	TGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGAGATTTAGCAGCC 2	TTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAG	TTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAG 2		GCAACCTCCGAGAATACCTCCGAGCCCGGGAGGCCACCCGGGATGGAGTACTCCTATGAC 2	TTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAA 1	TTCTTGGAGCCTGCACACAGGATGGGGCTCTCTATGTCATAGTTGAGTATGCCTCTAAA 1	ATCTGCTGTCAGAGATGGAGATGATGATGGGAAACACAAGAATATCATAAAT	ATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGAAACACAAGAATATCATAAAT 1	AGGCGGTCACCGTGGACGTGAAGATGTTGAAAGATGATGCCACAGAGAAAAGACCTTTCT	AGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAAGACCTTTCT 1	GTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGCAAAGCCCAAG	GTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCCAAG 1	AGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAGAA	AGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAGAA 1	GCCTCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCA	GCCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCA 1	TTTCGGCTGAGTCCAGCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA	TTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCCGCTGGTGAGGATAACAACA	

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; LOCATION: 25..1953
US-08-471-570-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIF: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOSTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING JAPE: 06-7UN-1955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1954 base pairs
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FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, Ernest V
REGISTRATION NUMBER: 29822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: IGARSHI, KOLCHI
APPLICANT: SENOO, Masaharu
APPLICANT: WATNANBE, TREBUYA
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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490 ACTAAGGATGGGGTCCACTTGGGGGCCCAACAATAGGACAGTGCTTATTGGGGAGTACTTG 549
                                                               181 GCGCCAGGGGAGTCGCTAGAGGTGCGCTGCTTGAAAGATGCCGCCGTGATCAGTTGG 240
                                                                                        430 GCGCCAGGGAGTCGCTAGAGGTGGGCTGCCTGTTGAAAGATGCCGCCGGTGATCAGTTGG 489
                                                                                                                                                       121 TTAGAGCCAGAAGAGCCACCAACCAAATACCAAATCTCTCAACCAGAAGTGTACGTGGCT 180
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61 GTCACCATGGCAACCTTGTCCCTGGCCCGGCCCTCCTTCAGTTTAGTTGAGGATACCACA 120
                                                                                                                                                                                                                                                                                                                                       29 GGACCGGGATTGGTACCGTAACCATGGTCACTGGGGTCGTTTGATCTGCTCGGTCGTG 309
1 GGACCGGGGATTGGTACCGTAACCATGGTCAGCGGGGTCGTTTGATCTTCATCTGCTGGTCGT6 60
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CITY: Boston
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1620 1374	GTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGCAACACACAC	1315	Db Qy
1314	HITTHITHITHITHITHITHITHITHITHITHITHITHIT	255	Db
1560	AGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAAC	501	ο ν
n o	TGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTC	1141	P 64
1194	AGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGC		Db
1440	ACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCC	1381	Qy
1134	ACAGCAAGCGCCTGGAAGAGAAAAGGAGAT	1075	Db
1380	ACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGG	1330	Qy
1074	ACCGAGGCGGATGCGGGGAATATATATGTAAGGTCTCCAATTATATAGGGCAGGCCAAC	1015	Db
1329	TITTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGGATATCCTTT	1270	Qy
1014	AGCACTCGGGGATAAATAGTTCCAATGCAGAAGTGCTGGCTCTTTCAATGTG	961	Db
1269	GGCCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATGTA	1210	Qy
960	CACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTC	901	Db
1209	ACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGCCTGCCCTACCTCAAGGTTCT	1150	Оу
900	GACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCCACATCCAGTGGATCAAG	841	ф
1149	ACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACAT	1090	Оу
840	CCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGA	781	Db
1089	CTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGG	1030	Qy
780	GTGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGATCG	721	Db
1029	TGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGCAGCGATC	970	Qy
N	CACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTATACCTGTGTG	661	Db
969	ACTGGAGCCTCATTATGGAAAGTGTGGGTCCCATCTGACAAGGGAAATTA	910	VQ
660	AAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAG	601	Db
909	ACGAAACCAG	850	γQ
600	ACACTGTCAAGTTTCGCTGCCCAGCCGGGGGAACCCAATGCCAACCATGCGGTGGCTG	541	Db
849	ACACTGTCAAGTTTCGCTGCCCAGCCGGGGGG	790	Qy
540	GCACCATACTGGACCAACACAGAAAAGATGGAAAAGCGGCTCCATGCTGTGCCTGCGGCC	481	Db
789	CACCATACTGGACCAACACAGAAAAGATGGAAAAGCGGCTCCATGCTGTGCCTGCGGC	w	γo
480	GATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAACAACAAGAGA	421	Db
729	ATGAGGATGACACCGATGGTGCGGAAGATTTTTGTCAGTGAGAACAGTAACAACAAGAG	670	Qy
2	GTAGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCATCCGGAGAT		Ф
669	AGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCATCCGGA	610	Qy
6		301	dd
609	AGATAAAGGGCGCCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCCAGTAGC	550	Qy
300	ACTAAGGATGGGGTGCACTTGGGGCCCCAACAATAGGACAGTGCTTATTGGGGGAGTACTTG	241	ф

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-100S
SOFTWARE: PAtentin Release #1.0, Version
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                           APPLICAMY: SENDO, MASAharu
APPLICAWY: MATNANBE, TAESUYA
TITILE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                       STREET: 130 W
CITY: Boston
STATE: Massac
COUNTRY: US
              FILING DATE:
                                                                  CLASSIFICATION: 435
                                                                                 APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                            ADDRESSEE: DAVID G. CONLIN; DIKE, ADDRESSEE: CUSHMAN
APPLICATION NUMBER:
                                                                                                                                                                                                                           ZIP:
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                                                                                                                                                                                                                           02109
                                                                                                                                                                                                                                                          Massachusetts
                                                                                                                                                                                                                                                                                         130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                    IGARASHI, Koichi
                                                                                   06-JUN-1995
US 07/743369
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Best Local Similarity
Matches 1778; Conserv
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2310 base pairs
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ATTORNEY/AGENT INFORMATION:
NAME: LINEK, ETNEST V
REGISTRATION NUMBER: 2982
REFERENCE/DOCKET NUMBER: 4089
TELEPHONE: [61]23-3400
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LOCATION:
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                               TTACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCG 1438
                                                                                                 TTCACTCTGCATGGTTGACACTTCTGCC-----AGCGCCTGGAAGAGAAAAGGAGA 1378
                                                                                                                                                                           TAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGGATATCCT 1327
                                                                                                                                                                                                                                                        TCAAGGCCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATG 1267
                                                                                                                                                                                                                                                                                                                           AGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTC 120
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                                                                                 ACCAGTCTGCCTGGCTCACTGTCCTGCCAAAACAGCAAGCGCCTGGAAGAGAAAAGGAGA
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                                                           CCAACGAACTGTACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAA 2518
                                      CCAACGAACTGTACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAA
                                                                                                                         TCGGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCG
                                                                                                                                                                                                                                                                                               GATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGATGTCTGGTCCT
                                                                                                                                                                                                                                                                                                                                      GGATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTGATGTCTGGTCCT 2338
                                                                                                                                                                                                                                                                                                                                                                                   GAGATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGT
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US-08-070-165F-5
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US-08-070-165F-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
TELECHMINICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEPHONE: (614)-293-8093
TELEPHONE: (614)-293-5631
INCOMMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Ing-Ming Chiu
STREET: $2052 Davis Medical Research Center, 48
STREET: 9th Avenue
CITY: Columbus
CITY: Ohio
COUNTRY: USA
ZIP: 43210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM. PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08070165F Patent No. 5750365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast
                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE: Meso
IMMEDIATE SOURCE:
LIBRARY: lambda
CLONE: KP23-1
         JOURNAL: Biochim. Biophys
VOLUME: 1220
PAGES: 209-211
DATE: 1994
RELEVANT RESIDUES IN SEQ I
                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME:
UNITS: bp
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                        PUBLICATION INFORMATION
                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                     LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Regenerating f
CELL TYPE: Mesenchyme and F
                                                                                                   AUTHORS: Poulin, Matthew L
TITLE: Nucleotide sequences of two newt
TITLE: (No. 575055cphthalmus viridescens) fibroblast growth
TITLE: factor receptor-2 variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2675 base pai
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: No. 5750365ophthalmus viridescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/070,165F FILING DATE:
                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                             : Lambda gtll
KP23-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2675 base pairs
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2512..2675
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325..2511
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Epithelium
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GTATGAACTTCCAGAGGACCCCAAAATGGGAGTTTCCCAAGAGATAAGCTGACACTGGGCAA 1727	1668	Ş
GATCACCACTCGCCTGTCTTCCAACAATGACACCCACTTGCTGGCCGGGGTCTCCG	1383	₽
AGGATAACA	60	Qy
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AGGTAACAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGGCTGG	1548	ó
GAAGCCAGACTTCAGCAGCCAGCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCG 1547	1488 1263	рь
TTCCTGATCACCTGCATGATTGGCACAATCATGGTGTGCCACATGAAGGGCAGAGGCAA 126	20	Db
CTTCTTAATCGCCTGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAA 1487	1428	γ
	14	Db
aggagattacagcttccccagactacctggagatagccatttactgcatagc	1368	Q Q
TAATTCTACTGGGATATCCTTTCACTCTGCATGGTTGAAGATTCTGCCAGGGCGCCTGGAAG 1367	1308	D 04
CTCTATGTGCGCAATGTCTCTTTTGAGGATGCTGGGGAGTATACGTGCTTGG	1029	В
GGTTCTCTATATTCGGAATGTAACCTTTTGAGGACGCCTGGGGAATATACGTGCTTGGCGGG 1307	1248	Qy
GCATCCCTATCTGAAAGTGCTAAAGGCGGCCGGTGTTAACACCACGGACAAAGAGATCGA 1028	969	Дb
ACCTCAAGGTTCTCAAGGCCGCCGGTGTTAACACCACGGACAAAGAC	1188	γQ
GCCACATATCCAATGGATTCGACATTTTGAGCTGAATGGCAGTAAAATTGGACCTGACGG 968	909	당
CCACATCCAGTGGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGA	1128	Q
	849	рb
CTCCACAGTGGTCGGAGGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGA1	1068	Ş
4	78	당
CTGGATGTTGT6GAGCGATCGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAA 10		Ş
CGAGGGCAACTACACCTGTATCATGGAGAACGAGTATGGATCCATCAATCA	729	D <sub>D</sub>
AAGGGAAATTATACCTGTGTGGTGGAGAATGAATACGGGTCCATCAATCA	948	Q
GGCTTCAAGGTACGTAGTCAACACTTCAGCCTGATCATGGAGAGGGTGGTTCCCTCTGA 72	6	Db :
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TACGCCCTCCATGAGGTGGCTGAAGAACGGCAAGGAGTTCAAGCAGGACCACCGCATTGG 668	0 .	g 5
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CATGCTGTGCCTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGGAACC	768	Ş
TGACAACAACCACATGAGGGCTCCGTACTGGACGAATACAGAAAAATTGGAAAAGAA 548	492	Ъ
GAGAACAGTAACAACAAGAGAGCACCATACTGGACCAACACAGAAAAGATGG	708	9
CAAACTCATCAGGGGATGATGAAGACGACGACGACGGCTCGGAAGATTTCACAAA 49	432	Db 5
ATOCHATOROPAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		-
tch 32.0%; Score 1367.6; DB 1; Length 2675; abl Similarity 79.1%; Pred. No. 0; 154; Conservative 0; Mismatches 429; Indels 9; Gaps	uery Ma est Loc latches	<b>3</b> 0 0

Db Qy	Db	Qу	о <sub>у</sub>	DЪ	Qy	Db 4	Ş	Db Qy	Db	οy	Db	γO	Db	γo	Db	νο	Db	ογ	Db	γo	В	9	Db	Qγ	ДĎ	Оу	DЬ	Оу	망	Ωу	DЬ
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CGARCCATGCCTTCCTCAGATATCCACACTAAACGCCAGTGTTAAAACATGA 2739 		AGAAGTTCTTGTTCTTCAGGAGATGATTCTGTTTTTTTCTCCAGACCCCATGCC	CANTGAGGANTACTTGGACCTGAGCCAACCTCTGGAACAGTATTCACCTAGTTACCTGGA	GCAAAGACCCACTTTCAAGCAGCTTGTTGAGGATCTAGACCGAATCCTCACGCAAACGAC	agagaccaacgitcaagcagtiggtagaagactiggatcgaattctcactctcac	TGGCAACTGCACCAATGAGCTGTATACAATGATGACGGACTGCTGGGCTGTGCCCTC 2	CONDA COME COORTANTA COOR ON SOME ON COMBONICA COOR A COOR A COORTANTA COMBONICA COORTANTA COMBONICA COORTANTA	AGGATTCCCGTGGAGGAACTTTTTAAGCTGCTGAAGGAAG	CGTCTGGTCTTTCGGTGTGCTTATGTGGGAGATCTTCACACTGGGGGGTTCCCCATACCC	STCCTTCGGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCC	CCCCGTGAAGTGGATGGCTCCCGAGGCGCTGTTTGACAGAGTCTACACACAC	CAGTCAAGTGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAGTG	TGGTTTGGCCCGAGACATCAACAACATCGACTACAAAAAAAA	actogocagagatatcaacaatata	GACTTGGCAGCTCGGAATGTCTTGGTGACGGAAACCAACGTCATGAAAATTGCAGATTT 1	AGATTTAGCAGCCAGAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGACTT 2	TTGCACGTACCAACTGGCCAGGGGAATGGAGTACCTGGCATCAGAGAAGTGCATCCATC	A.	GTACTCCTTTGACATCAACAGAATTCCTGAAGAGCAGATGACCTTCAAGGACCTAGTGTC	TACTCCTATGACATTAACCGTGTTCCTGAGGAGCAGATGACCTTCAAGGACTTG	ATATGCCTCCAAGGGAACTTGCGTGAATACTTGCGCACCCGCCGACCTGGCATGA	CCTCTAAAGGCAACCTCCGAGAATACCTCCGAGCCCGGAGGCCACCCGGGATGG	AAATATCATCAATCTTCTAGGAGGGTGCACCCCAAGATGGCCCACTCTACGTGATAGTCGA	ATCATAAATCTTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTG	GAAGGATCTTTCTGATCTCGTGTCTGGGAGATGGAAATGATGAAGATGATTGGGAAGCATAA	AAAGACCTTTCTGATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGAAACAC	ACCGTGG	CAAGCCCAAGGAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAG	TGGGCGAAGGCTGCTTTCGGGCAGGCTGGTGATGGCAGAGGCGGTGGGCAT	CCCTGGGAGAAGGTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGAC	
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TOPLOGY: linear
HOLECULE TYPE: CONA
HYPOTHETICAL; NO
ANTI-SENSE: NO
ORGINAL SOURCE:
ORGANISM: No. 59252Bophthalmus viridescens
DEVELOPHENYAL SYADE: Adult
"TESUE TYPE: Regenerating forelimb blastema"
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                                            Query Match
Best Local Similarity
Matches 1654; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (614)-293-8093
TELEPAX: (614)-293-5931
INFORMATION FOR SEQ ID No: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08885418 Patent No. 5925528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Chil, Ing-Ming
APPLICANT: Poulin, Matthew L
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
                                                                                                                                                                            NAME/KRY. 3/UTR
LOCATION: 2512: 2675
PUBLICATION INFORMATION:
AUTHORS: POULIN, Matthew L
TITLE: Nucleotide sequences of two newt
TITLE: (No. 5925280phthalmus viridescens) fibroblast growth
TITLE: (No. 5925280phthalmus viridescens) fibroblast growth
TITLE: factor receptor-2 variants
JOHRAL: BIOPHM. BIOPHYS. Acta
VOLUME: 120
PACES: 209-211
PACES: 209-211
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MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACEDLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/885,418
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Ing-Ming Chiu
STREET: $2052 Davis Medical Research Center, 480 West
STREET: $105 Lavenue
CITY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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UNITS: bp
648 AGATGCCATCTCATCCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAG 707
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                                                                                                                                  DATE: 1994
RELEVANT RESIDUES IN SEO ID NO: 5: FROM 1 TO 2675
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 325..2511
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LOCATION: 1..324
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                                               Conservative
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                                                             32.0%;
                                                             Score 1367.6;
Pred. No. 0;
                                         Mismatches 429;
                                                                                DB 2;
                                         Indels
                                                                           Length 2675;
                                         9; Gaps
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1787	28 GCCCCTGGGAGAAGGTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAA	0у 17	
1502	43 GTATGAGCTGCCAGAGGACCCCAAGTGGGAGTATCCAAGGGAAAAGCTCACGCTGGGGAA	Db 14	
1727	TATGAACTTCCAGAGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGG	0y 16	
1667 1442	08 GAGGATRACAACACGCTCTCTCAACGACACACCCCATGCTGGCAGGGGTCTCCGA 111   1   1   11   1   1   1   1   1	Oy 16	
1607 1382	8 GAGACAGGTAAC 	13	
1547 1322	8 GAGCCAGACTTCAGCAGCCAGCCGGCTGTGCACAAGCTGACCAAACGT	12	
1262	3 CTTCCTGATCACCTGCATG	12	
1202	GAACTGGATTCATCATCGGAGTATACGGAAATCGCCATCTACTGTGTGGGA	: :	
1427	AAAGGAGATTACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGC	0у 13	
1367 1148	### TAPTICTATION OF THE PROPERTY OF THE PROPER	Db 10	
1088	AGTCCTCTATGTCCGCAATGTCTTTTTTGAGGATGCTGGGGAGTATACGTGCTTGGG		
1307	TCTCTATATTCGGAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGC	0у 12	
1247 1028	B CCTGCCTACCTCAAGTTCTCAAGCCCCCCGGTGTTAACACCACGGACAAAGATTGA	Оу 11 Db 9	
968	09 GCACATATCCAATGGATTCGACATTTTGAGCTGAATGGCAGTAAAATTGGACCTGACGG	Db 9	
1187	CCCCACATCCAGTGGATCAAGCAGGTGGAAAAGAACGGCAGTAAATACGGGCCCGAC	Oy 11	
806	49 CACAACCACAAAAGTTGGGGGCGATGCAGAGTTTGTTTGCAAAGTCTACAGTGAC		
_	68 TGCCTCCACAGTGGTCGGAGGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGC	Qy 10	
1067 848	08 CCTGGATGTTGTGGAGGGATGGCCTCACCGCCCATGCTCCAAGCCGGACTGCCGGCAAA 101	Qy 10 Db 7	
788	29 CGAGGGCAACTACACCTGTATCATGGAGAACGAGTATGGATCCATCAATCA	Db 7	
1007	48 CAAGGGAAATTATACCTGTGTGGGGGGGGAGATGAATACGGGTCCATCAATCA	Оу 9	
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947	88 AGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCT	Оу 8	
	09 TACGCCCTCCATGAGGTGGCTGAAGAACGGCAAGGAGTTCAAGCAGCAGCACCGCATTGG	Db 6	
887	28 ANTGCCAACCATGCGGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTG	Оу 8	
808	49 ACTCCATGCTGTGCCCGCTGCCAACACTGT	-	
827	68 GCTCCATGCTGTGCCTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGGAACC	Qy 7	
548	92 TGACAACAACCACATGAGGGCTCCGTACTGGACGAATACAGAAAAAATTGGAAAAAGAA	Db 4	
491	32 AGATGCAAACTCATCAGGGGATGATGAAGACGACGACGGCTCGGGAAGATTTCACAA		

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                                                                                              RESULT 8
                         Sequence 3, Application US/08471570 Patent No. 5750371 GENERAL INFORMATION:
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APPLICANT: IGARASHI, Koichi
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                                                                                                                                                                     CGAACCATGCCTTCCTCAGTATCCACACATAAACGGCAGTGTTAAAACATGA 2739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTATGCCTCTAAAGGCAACCTCCGAGAATACCTCCGAGGCCCGGAGGCCACCCGGGATGGA 2027
                                                                                                                                              CGACCCCTGTCTTCCCAAATCCCAACACACAAACGGCACCATTAAAACATGA
                                                                                                                                                                                                              TACCAGGAGTTCCTGCTCTTCTGGGGATGACTCTGTCTTCTCCCCGGACGCAATGCCCCTA
                                                                                                                                                                                                                                 CACAAGAAGTTCTTGTTCTTCAGGAGAGGATGATTCTGTGTTTTTTTCTCCAGACCCCATGCCCTTA
                                                                                                                                                                                                                                                                            CAATGAGGAGTACCTGGACCTCAACAACCCTCTGGAGCAGTACTCGCCGAGCTATCCGGA
                                                                                                                                                                                                                                                                                                 CAATGAGGAATACTTGGACCTCAGCCAACCTCTCGGAACAGTATTCACCCTAGTTACCCTGA
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APPLICATION NUMBER: US 07/743
APPLICATION NUMBER: 1991
APPONENT NUMBER: 29822
RECEPTANTON NUMBER: 29822
REFERENCE/DOCKET NUMBER: 4089
TELECOMMUNICATION LYFORMATION:
TELECY 100291 STRE UR
INFORMATION FOR SED ID NO: 3
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION
CURRENT APPLICATION DATA:
APPLICATION UNUBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SENOO, MASSHATU
APPLICANT: WATANABE, TACKSUA
TITLE OF INVENTION: PROTEIN, DNA
NUMBER OF SEQUENCES: 18
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CITY: Boston
STATE: Massac
COUNTRY: US
ZIP: 02109
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DAVID G. CONLIN;
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                  Match 30.9%;
Local Similarity 94.7%;
               CGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAG
                                                                                                                                                                                                                                                               CCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGGAACCCAATGCCAACCATGCGGTGGC
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  CGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAG
                                                                                          TGGTGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGAT 1021
                                                                                                                                                                                                                  TGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACC
                                                            TGGTGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGAT
                                                                                                                        AGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTATACCTGTG
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Pred. No. 2.7e-314;
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US-08-070-165F-9
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Patent No.
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                                                                                                                                                                                                                                                                                                                     CLONE: KP19-1
POSITION IN GENOME:
UNITS: bp
FEATURE:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                  NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPALIBLE

OPERATING SYSTEM: PC-005/MS-DOS

SOFTMARE: Patentin Release #1.0, Version #1.25

APPLICATION DATA: US/08/070,165F
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: Regenerating forelimb blastema CELL TYPE: Mesenchyme and Epithelium IMMEDIATE SOURCE:
LIBRARY: lambda gtl1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (614)-293-8093
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chio, Ing.Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2159 CCAGAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAG
                                                                                                                                                   PUBLICATION INFORMATION:
AUTHORS: Poulin, Matt
                                                                                                                                                                                                                                                                    LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
ANTI-SENSE: I
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                                                                        AUTHORS: Chiu, Ing-Wing
TITLE: Nucleotide sequences of two newt
TITLE: (No. 5750355phthalmus viridescens) fibroblast growth
TITLE: factor receptor 2 variants
                  PAGES: 209
DATE: 1994
                              JOURNAL: Biochim. Biophys. Acta
VOLUME: 1220
PAGES: 209-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: No. 5750365ophthalmus viridescens DEVELOPMENTAL STAGE: Adult
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TOPOLOGY: lir
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U:
ZIP: 43210
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STREET: S2052 Davis Medic
STREET: 9th Avenue
CITY: Columbus
RELEVANT RESIDUES
                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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ş ş В Ş 밁 8 밁 무 9 Q. В Ş 망 Ş 망 9 Вρ á â 밁 В 망 Ş Š 밁 9 В 밁 9 S 8 В В Ş US-08-070-165F-9 Query Match 29.9%; Best Local Similarity 76.6%; Matches 1607; Conservative 1383 1602 1323 1422 1542 1263 1482 1203 1143 1368 1083 1023 1248 1188 1128 1068 1008 969 909 849 789 729 948 669 888 609 828 549 492 708 648 AGATGCCATCTCATCCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAG 707 GCTGGTGAGGATAACAACACGCCTCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGT 1661 TGCCTCCACAGTGGTCGGAGGAGAGAGTTTGGTCTGCAAGGTTTACAGTGATGCCCA 112 ACTGGTCCGGATCACCACTCGCCTGTCTTCCAACAATGACACCCACTTGCTGGCCGGGGT 1442 CCTGCGCAGACAGGTAACAGTGTCTGCTGACTCCAGCTCTTCTATGAACTCCAACACTCC 1382 CCTGCGGAGACAGGTAACAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCC 1601 AGGCAAGAAGTCTGACTTCAGCAGCCCACCCGCTGTGCACAAGCTGAGCAAGAGTCTCCC 1322 GACCAAGAAGCCAGACTTCAGCAGCCAGCCAGGCTGTGCACAAGCTGACCAAACGTATCCC 154: GGGAGGCTTCCTGATCACCTGCATGATTGGCACAATCATGGTGTGCCACATGAAGGGCAG 1262 AGGGGTCTTCTTAATCGCCTGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACAC 1481 AGATGAAGAACGGGAACTGGATTCATCATCGGAGTATACGGGAAATCGCCATCTACTGTGT 1202 -----AGAAAAGGAGATTACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCAT 1421 TAATTCTATTGGGATATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAG 1367 AGTTCTGACCCTGCATAACGTGACTGAGGCGGACCGGGGCCCAGTACACATGCAAAGTCTC 1082 GGTTCTCTATATTCGGAATGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGG 1307 GCATCCCTATCTGAAAGTGCTAAAGCGCTCTGGAATTAATAGCTC-----CAATGCCGA 1022 GCTGCCCTACCTCAAGGTTCTCAAGGCCGCCGGTGTTAACACCCACGGACAAAGAGATTGA 1247 GCCACATATCCAATGGATTCGACATTTTGAGCTGAATGGCAGTAAAATTGGACCTGACGG 968 GCCCCACATCCAGTGGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGG 1187 CCTGGATGTTGTCGAGCGGTCACCCCACCGGCCAATACTCCAAGCTGGGCTTCCGGCAAA 848 CCTGGATGTTGTGGAGCGATCGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAA 1067 CGGCTTCAAGGTACGTAGTCAACACTTCAGCCTGATCATGGAGAGCGTGGTTCCCTCTGA 728 AGGCTACAAGGTACGAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGA 947 TACGCCCTCCATGAGGTGGCTGAAGAACGCCCAAGGAGTTCAAGCAGGAGCACCGCATTGG 668 AATGCCAACCATGCGGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGG 887 TGACAAC---AACCACATGAGGGCTCCGTACTGGACGAATACAGAAAAATTGGAAAAAGAA 548 TGAGAACAGTAACAACAAGAGCACCATACTGGACCAACACAGAAAAGATGGAAAAGCG 767 AGATGCAAACTCATCAGGGGATGATGAAGACGACGACGACGGCTCGGAAGATTTCACAAA 491 Score 1276.4; DB 1; Length 2681; Pred. No. 8.6e-304; O; Mismatches 476; Indels 15; 15; Gaps 788 w \

82 GCCTTACGAACCATGCCTCAGTATCCACACATAAACGGCAGTGTTAAAACATGA 2739 	2682 2463	oy da
22 CCURGACAMGANGTYCTYGTYCTTCARGAKANGAYTCTGTTTTTTTCCCAGCCCCAT 2681   1	2622 2403	Db Qy
	2562 2343	p oy
3 GCCCTCCARGACCCAACGTTCARGCAGTTGGTAGAAGACTTGGTAGAATTCCTARTCCTCT 2561	2502 2283	Db
2 TAMGCCAGCCAACTGCACCAACGAACTGTACATGATGATGAGGGACTGTTGG	2 4	DЬ
31 CTACCCAGGGATTCCCGTGAAGAACTTTTTAAGCTGCTGAAGGAAG	16	D Qy
22 GAGTGATGTCTGGTCCTTCGGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGCCTCGCC 2381	10	Оb
62 GCGGCTTCCAGTCAAGTGGATGGCTCCCAGAAGCCCTGTTTGGTAGAGTATACAGTATACAGTATACA 43 CCGGCTCCCCGTGAAGTGGATGGCTCCCGAAGGCGCTGTTTGACAAGAGTCTACAGACATCA 43 CCGGCTCCCCGTGAAGTGGATGGCTCCCGAAGGCGCTGTTTGACAAGAGTCTACAGACACTCA 2102	2 2	Db Oy
02 AGACTITGGACTCGCCAGAGATATCAACAATATAGACTATTACAAAAAGACCACCAATGG 2261 	220 <b>2</b> 1983	Db Db
42 TCATCAGAGATTAGCAGCAGAAATGTTTTGGTAACAGAAAACAATGTGATGAAAAAGG 2201 1111   1   1   1   1   1   1   1   1	92	Оy
83 GRITICATICACCIACCACCACCACACACACACACTICACTITICCCAAAAATCATA 2141   1111	96	Qу
22 GATGGAGTACTCCTATGACATFAACCGTGTTCCTGAGGACCAGGATGACCTTCAAGGACTT 2081 	80	Оy
62 AGTTGGAFFATGCCTETMAAGCAACCTCCGAGAATAACTCCCAGCCGGAGCCGAGCC	1962 1743	DP 6À
02 ACACAAGAATATCATAAAPTTCTTGGAGCCTGCAACACAGGATGGGCCTCTCTATGTAT 1961 	90	Db Oy
42 CACAGAGAAAGACCTTTCTGATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGAA 1901 	1842 1623	рь
82 TGAGAAAGACAAGCCCAAGGAGGCGSTCACCGTGGCCGTGAAGATGTTGAAAGATGATGC 1841 	56	Оy
22 GGCAMACCCCTGGGAGAMGTTGCTTTGGGAMGTGGTGATGGGGAMGCGGTGGAAT 1781 23 GGGAMGCCCTGGGGCAMAGGTGCTTTGGGAMGTGTGATGAGAGGGGGAMGCGTGGGAAT 1781 24 GGGAMGCCCTGGGCGAMGGCTGCTTCGGGCAGGTGGTGATGGCAGAGGCGGTGGGATT 1562	50	pb dy
62 CTCCGAGTATGAACTTCCAGAGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACT 1721 	1662 1443	Оу

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RELEVANT RESIDUES IN SEQ ID NO: 9: FROM 1 TO 2681 US-08-885-418-9
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TELECOMMUNICATION INFORMATION:
TELEPRONE: (614)-293-8631
TELEPRONE: (614)-293-8631
INFORMATION FOR SEO ID NO: 9:
SEQUENCE GRANACTERISTICS:
LEACH: 2661 Date PallTS
TYPE: INFORMATION FOR SEO ID NO: 9:
PARADEDRESS: QUIBBLE
TYPE: TRANDEDRESS: QUIBBLE
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08885418 Patent No. 5925528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: NO. 5925280phthalmus viridescens
DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Regenerating forelimb blastema
CELL TYPE: Mesenchyme and Epithelium
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GERERAL INFORMATION:
APPLICANT: Chin, Ing-Ming
APPLICANT: Chin, Ing-Ming
Ing-Ming L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1.324
FEATURE:
NAME/KEY: CDS
LOCATION: 325.2517
FEATURE:
                                                                                                                                                                                                                                        NAME/KEY: 3'UTR
NAME/KEY: 3'UTR
LOCATION: 2518..2681
LOCATION: INFORMATION:
AUTHORS: Poulin, Matthew L
AUTHORS: Chiu, Ing-Ming
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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UNITS: bp
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TYPES: 209-211
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                                                                                                                                                                TITLE: Nucleotide sequences of two newt
TITLE: (NO. 59255280phthalmus viridescens) fibroblast growth
TITLE: factor receptor 2 variants
JORNAL: Blochim. Blophys. Acta
                                                                                                          PAGES: 209
DATE: 1994
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Ing-Ming Chiu
STREET: S2082 Davis Medical Research Center, 480 West
STREET: 9th Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY:
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76.68;
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Score 1276.4; DB 2; Length 2681; Pred. No. 8.6e-304;
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g Qy	Db Oy	Db 09	Db Qy	B 8	о О	Ωу	Оy	pb Qy	Ωу Въ	Оу	ОУ	Db Qy	Оy	Qу	Оy	Оy	Оу	ма
1662 1443	1602 1383	32	1482 1263	1422	1368 1143	1308 1083	1248 1023	969	1128 909	1068 849	1008 789	948 729	669	828 609	768 549	708	648 432	ō
CTCCGAGTATGAACTTCCAGAGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACT 1	GGT 1		AGCCAAGAAGCCAGACTTCAGCAGCCAGCCGCTGTGCACAAGCTGAGCCAAAGCTTACCCAAGCTGAGCAAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	GGGAGGCTTCCTANTCACCTGCATGATTAGCACATCATCGTGTGCCAATGAAGAGACACACAC	GT 1	TCTATTGGGATATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAG 1 	GETTCTCTATATTCGGGAATGTAACTTTTGAGGGGACCGTGGGGGAATATGAGCGTTGGCGGG 1	GCTGCCCTACCTCAAGGTCTCAAGGCCCCGCCGTGTTAACACCACGGACAAAAGAGATTA GCTGCCCTACCTCAAGGTCTCAAGGCCCCCGCGATTAACACCACGGACAAAAGAGATTA GCATCCCTATCTGAAAGTCCTAAAGCGCTCTGGAATTAATAGCTCCAATGCCGA	GCCCCACATCCAGTGGATCAAGCACGTGGAAAGAAGAGGGCAGTAAATACGGGCCCGACGG 1	TGCCTCCACAGTGGTCGGAGGAGACGTAGAGTTTGTCTCCAAGGTTTAGAGTGATGGCCA 1	CCTGGATGTTGTGGACGGATCGCCTCACCGGCCATCCCAAGCCGACTGCGACTGCGCAAAAAAAA	CARGGGAATTATACCTGTGTGGGGAGAATGAAATGACAGGGTCCATCATGACAGGTACCA   1  1  1  1  1  1  1  1  1  1  1  1  1	AGGETACAAGGTAGGAAACCAGGACGGAGCCTCATTATGGAAAGGTGGTCCCATTCAT 	AATGCCAACCATGCGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGG 8	GUTCANGCTGTGCCTGCGGCCAAAAACTGTGAAGTTCCGCTGCCAGCGGGGGGGAAAACTGTGTAAGTTGCTGCTGCCAGCGGGGGGAAAACTGTGAAGTTCGGCTGTCAAGCGGTGGCAACAC	TGAGAACAGTAACAACAAGAAGCACCATACTGGACCAACACAGAAAAGGAAGG	AGATGCAACTCTCATCAGGGAGATGATGAGGAGGACGCGGAGAGGTTTGCGAAAA 4 AGATGCAAACTCATCATCAGGGGATGATGATGAGAACAACGACAACGACGGCTCGGAAGATTTCACAAA 4	G
721 502	661 442	601 382	541 322	481 262	421 202	367 142	307 082	247 022	187	1127 908	067	007	28	68	27	67	91	ps

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RESULT 11
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1503 GGGGAAGCCCCTGGGCAAGGCTGCTTCGGGCAGGGCAGTGGTATTGGCAAGAGGGGTGGCAT 1562
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                                                                                                                                         GCCTTACGAACCATGCCTTCCTCAGTATCCACACATAAACGGCAGTGTTAAAACATGA 2739
                                                                                                                                                                                                  CCCTGACACAAGAAGTTCTTGTTCTTCAGGAGATGATTCTGTTTTTTTCTCCAGACCCCAT 2681
                                                                                                                                                                                                                                                                                       CACAACCAATGAGGAATACTTGGACCTCAGCCAACCTCTCGAACAGTATTCACCTAGTTA 2621
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                                                                                                       GCCCTACGACCCCTGTCTTCCCCAAATCCCCAACACACAAACGGCACCATTAAAACATGA 2520
                                                                                                                                                                             TCCGGATACCAGGAGTTCCTGCTCTTCTGGGGATGACTCTGTCTTCTCCCCGGACGCAAT 2462
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                                                                                                                                                                                                                                                                                                                                 GCCCTCGCAAAGACCCACTTTCAAGCAGCTTGTTGAGGATCTAGACCGAATCCTCACGCA 2342
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STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: [
US-07-997-133-2
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Best Local Similarity
Matches 1616; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1755 Jefferson Davis Highway, Fourth Floo
CITY: Arington
STATE: Virginia
ZIP: 2200
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC COMPACTURE
OPERATING SYSTEM: DC-005/M5-DOS
SOFTWARE: PALEONIA DATA
RESET APPLICATION NORTH STATE
OF THE CONTROL OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)221-4500
TELEFAX: (703)486-2347
TELEX: 24885 DAT UR
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5288855man F.
REGISTRATION NUMBER: 24,618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Extracellular Form of the Human TITLE OF INVENTION: Fibroblast Growth Factor Receptor NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bergonzoni
APPLICANT: Mazue, Guy
APPLICANT: Isacchi, Ar
APPLICANT: Roncucci, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                            638 TGAATGTCACAGATGCCATCTCATCCGGAGATGATGAGGATGACACCGATGGTGCGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OBLON, SPIVAK, McCLELLAND, ADDRESSEE: P.C.
CATCCCCAGAAAAGATGGAAAAGAAATTGCATGCAGTGCCGGCTGCCAAGACAGTGAAGT
                                                                   CCAACACAGAAAAGATGGAAAAGCGGCTCCATGCTGTGCCTGCGGCCAACACTGTCAAGT 802
                                                                                                                                                 CAGAGGAGAAAGAAACAGATAACACCAAACCGTATGCCCGTAGCTCCATATTGGA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAGACAGTGAAACTTGGTACTTCATGG 637
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                                                                                                                                                                                                                          ATTTTGTCAGTGAGAACAGTAACAACAA-------GAGAGCACCATACTGGA 742
                                                                                                                                                                                                                                                                                                   TCAATGTTTCAGATGCTCTCCCCTCCTCGGAGGATGATGATGATGATGATGACTCCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGGCCTCTATGCTTGCGTAACCAGCAGCCCCTCGGGCAGTGACACCACCTACTTCTCCG
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Roncucci, Romeo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 1.1e-280;
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GCCACAGAGAAAGACCTTTCTGATCTGGTGTCAGAGATGGAGA 1882 	3 AGATGTTGAAAGATGATGCCACAGAGAAAG 	182 154
ATTGACAAAGACAAGCCCAAGGAGGCGGTCACCGTGGGCGTGA 1822 	3 TGGCGGAAGCAGTGGGAATTGACAAAGAC 	176 148
AGCTGACACTGGCAAGCCCCTGGGGACAAGGTTGCTTTGGGGCAAGTGCTA 1762   III   I	3 CAAGAGAT	170 142
GTCTCCGAGTATGAACTTCCAGAGGACCCAAAATGGGAGTTTC 1702 	3 CCCCATGCTGGCAGGGGTCTCCG	164 136
CCGCTGGTGAGGATAACAACACGCCTCTCTCAACGGCAGACA 1642	3 CCATGAACTCCAACACCCCGCTGGTGAGGA:               CCATGAACTCTGGGGTTCTTCTGGTTCGGCC	158
CCCCTGCGGAGACAGGTAACAGTTTCGGCTGAGTCCAGCTCCT 1582 	3 AGCTGACCAAACGTATCCCCCTGCGGAGAC 	152 124
ACGACCAAGAAGCCAGACTTCAGCAGCCAGCCGGCTGTGCACA 1522            GGTACCAAGAAGAGTGACTTCCACAGCCAGATGGCTGTGCACA 1246	3 TGTGCCGAATGAAGAACACGACCAAGAAG 	146 118
NTAGGGGTETTCTTAATCGCCTGTATGGTGGTAACAGTCATCC 1462 	3 AGATAGCCATTTACTGCA                    7 AGATCATCATCTATTGCA	112
CCTGGAAGAGAAAAGGAGATTACAGCTTCCCCAGACTACCTGG 1402	3 TGACAGTTCTGCCAGCGCCTGGAAGAGAAA                   7 TGACCGTTCTGGAAGCCCTGGAAGAGAGAGAG	Ο ω
TTGGCGGGTAATTCTATTGGGATATCCTTTCACTCTGCATGGT 1342 	3 CTGGGGAATATACGTGCTTGGCGGGTAATT 	128 100
GAGATTGAGGTCTCTATATTCGGAATGTAACTTTTGAGGACG 1282 	3 TTAACACCACGGACAAAGAGATTO	122 94
CCCGACGGCTGCCCTACCTCAAGGTTCTCAAGGCCGCCGGTG 1222	3 ACGGCAGTAAATACGGGCCCGACGGGCTGG 	116 88
GATGCCCAGCCCACATCCAGTGGATCAAGGACGTGGAAAAGA 1162 		8: 8:
CCGGCAAATGCCTCCACAGTGGTCGGAGGAGAGACGTAGAGTTTG 1102	3 TCCTCCAAGCCGGACTGCCGGCAAATGCC 	104 76
ACGTACCACCTGATGTTGTGGAGCGATCGCCTCACCGGCCCA 1042	83 ACGGGTCCATCAATCACACGTACCACCTGGA 	71
CCATCTGACAAGGGAAATTATACCTGTGTGGTGGAGAATGAAT	23 TTATGGAAAGTGTGGTCCCATCTGACAAGGG 	g yg
CGCATTGGAGGCTACAAGGTACGAAACCAGGACTGGAGCCTGA 922 	TGGAGGCT          TGGAGGCT	5 8
SGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAGG 862 	GAACCC 	y, ao

	CGTCTTCTCTCATGAGCCCCTGCCTACGAGCATGCCTTCCTCAGTATCA 2712    I   I   I   I   I   I   I   I   I	2381	B &
2380	ACCAGTACTCCCCCAGCTTTCCCGACACCCGGAGCTCTACGTGCTCCTCAGGGGAGGATGT	2321	B
2659	AACAGTATTCACCTAGTTACCCTGACACAAGAAGTTCTTGTTCTTCAGGAGATGATT	2603	Οy
2320	TGGACCGCATCGTGGCCTTGACCTCCAACCAGGAGTACCTGGACCTGTCCATGCCCCCTGG	2261	Db
2602	TGGATCGAATTCTCACTCTCACAACCAATGAGGAATACTTGGACCTCAGCCAACCTCTCG	2543	Qy
2260	GGGACTGCTGGCATGCCACTCACAGAGACCCACCTTCAAGCAGCTGGTGGAAGACC	2201	Db
2542	GGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACGTTCAAGCAGTTGGTAGAAGACT	2483	Оу
2200	AGGAGGGTCACCGCATGGACAAGCCCCAGTAACTGCACCAACGAGCTGTACATGATGATGATGC	2141	Db
2482	AGGAAGGACACAGAATGGATAAGCCAGCCAACTGCACCAACGAACTGTACATGATGATGA	2423	Qy
2140	TCACTCTGGGCGGCTCCCCATACCCCGGTGTGCCTGTGGAGGAACTTTTCAAGCTGGTGA	2081	뭥
2422	TCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCCGTGGAGGAACTTTTTAAGCTGCTGA	2363	Qγ
2080	ACCGGATCTACACCCACCAGAGTGATGTGTGTGTCTTTCGGGGTGCTCCTGTGGGAGATCT	2021	Дb
2362	ATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTCGGGGTGTTAATGTGGGAGATCT	2303	9
2020	ATAAAAAGCCAACCGCCCGCTGCGAAGTGGATGGCACCCGAGGCATTATTTG	1961	₽
2302	ACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGGATGGCTCCAGAAGCCCTGTTTG	2243	VΩ
1960	ACAATGTGATGAAGATAGCAGACTTTGGCCTCGCACGGGACATTCACCACATCGACTACT	1901	Ъ
2242	ACAATGTGATGAAAATAGCAGACTTTGGACTCGCCAGAGATATCAACAATATAGACTATT	2183	δÃ
1900	TGGCCTCCAAGAAGTGCATACACCGAGACCTGGCAGCCAGGAATGTCCTGGTGACAGAG	1841	рь
2182	TGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCCAGAAATGTTTTGGTAACAGAAA	2123	Qγ
1840	AGCTCTCCTCCAAGGACCTGGTGTCCTGCGCCTACCAGGTGGCCCGAGGCATGGAGTATC	1781	망
2122	AGATGACCTTCAAGGACTTGGTGTGTATGCACCTACCAGCTGGCCAGAGGCATGGAGTACT	2063	Qy
1780	AGGCCCGGAGGCCCCAGGGCTGGAATACTGCTACAACCCCAGCCACAACCCAGAGGAGC	1721	рь
2062	GAGCCCGGAGCCCACCCGGGATGGAGTACTCCTATCACATTAACCGTGTTCCTGAGGAGC	2003	Qy
1720	ATGGTCCCTTGTATGTCATCGTGGAGTATGCCTCCAAGGGCAACCTGCGGGAGTACCTGC	1661	ф
2002	ATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAAGGCAACCTCCGAGAATACCTCC	1943	Qy
1660	TGATGAAGATGATCGGGAAGCATAAGAATATCATCAACCTGCTGGGGGCCTGCACGCAC	1601	В
1942	TGATGAAGATGATTGGGAAACACAAGAATATCATAAATCTTCTTGGAGCCTGCACACAGG	1883	δ

RESULT 12
US-08-459-296-1
US-08-459-296-1
Fatent No. 5670323
Fatent No. 5670323, Michael
APPLICANT: No. 5670323, Michael
APPLICANT: No. 5670323, Michael
APPLICANT: No. 5670323, Michael
APPLICANT: No. 5670323, Michael
TILLE OF INVENTION: POCRESS FOR DETECTION OF NEOPLASTIC
TITLE OF INVENTION: POCRESS FOR DETECTION OF NEOPLASTIC
UNMERS OF SEQUENCES: 2
CORRESPONDENCE ADDRESSE
CORRESPONDENCE ADDRESSE
CORRESPONDENCE ADDRESSE
STREET: 1155 Avenue of the Americas
STREET: New York
STATE: NY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 2469 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASKERO Version 2.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
            983
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 71.1 es 1616; Conservative
ACGGGTCCATCAATCACGTACCACCTGGATGTTGTGGAGCGATCGCCTCACCGGCCCA 1042
                                                                                                                                                                                                                                                                                         CCAACACAGAAAAGATGGAAAAAGCGGCTCCATGCTGTGCCTGCGGGCCAACACTGTCAAGT
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                                             TAATGGACTCTGTGGTGCCCTCTGACAAGGGCAACTACACCTGCATTGTGGAGAATGAGT
                                                                              AATTCAAACCTGACCACAGAATTGGAGGCTACAAGGTCCGTTATGCCACCTGGAGCATCA
                                                                                                                                                    AGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTCA
                                                                                                                                                                                                                             TTCGCTGCCCAGCCGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAGG
                                                                                                                                                                                                                                                                   CATCCCCAGAAAAGATGGAAAAGAAATTGCATGCAGTGCCGGCTGCCAAGACAGTGAAGT
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                                                                                                                                                                                               TCAAATGCCCTTCCAGTGGGACCCCAAACCCCACACTGCGCTGGTTGAAAAAATGGCAAAG
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Pred. No. 1.1e-280;
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Sequence 2, Application General Information: Applicant: Bergonz Applicant: Mazue, Teacch
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APPLICANT: Koncucci, Romeo
APPLICANT: Sernientos, Paolo
APPLICANT: Sernientos, Paolo
TITLE OF INVENTION: Extracellular Form of the Human
TITLE OF INVENTION: Fibroblast Growth Factor Receptor
NUMBER OF SEQUENCES: 8
            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OBLON, SPIVAK, MCCLELLAND,
ADDRESSEE; P.C.
STREET: 1755 Jefferson Davis Highway,
CITY: Arlington
STATE: Virginia
21P: 22202
                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                               FILING DATE: 28-DEC-1992
                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGTTTTTTCTCCAGACCCCATGCCTTACGAACCATGCCTTCCTCAGTATCCA 2712
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1755 Jefferson Davis Highway,
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; MOLECULE TYPE: DNA (genomic)
US-07-997-133-2
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REFERENCE/OCKET NUMBER: 769-7
REFERENCE/OCKET NUMBER: 7769-7
REFERENCE (700) 552-4500
REFERENCE (700) 466-237
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.7%;
mest Local Similarity 71.1%;
Matches 1616; Conservation
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STRANDEDNESS: unkn
                                 ACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTCAAGGCCGCGGTG 1222
                                                                                                                                                                                                                                                                              TCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGAGGACGTAGAGTTTG 110:
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                                                                                                                                                                                                                                                                                                                                                         ACGGCAGCATCAACCACACATACCAGCTGGATGTCGTGGAGCGGTCCCCTCACCGGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAACCAGCACTGGAGCCTCA 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCGCTGCCCAGCCGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAAACGGGAAGG
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ATGGGAGCAAGATTGGCCCAGACAACCTGCCTTATGTCCAGATCTTGAAGACTGCTGGAG
                                                                                                                        TGTGTAAGGTGTACAGTGACCCGCAGCCGCACATCCAGTGGCTAAAGCACATCGAGGTGA
                                                                                                                                                                              TCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAGTGGATCAAGCACGTGGAAAAGA 1162
                                                                                                                                                                                                                                             TCCTGCAAGCAGGGTTGCCCGCCAACAAAACAGTGGCCCTGGGTAGCAACGTGGAGTTCA 826
                                                                                                                                                                                                                                                                                                                                                                                                                        ACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGATCGCCTCACCGGCCCA 1042
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FILING DATE: 18-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, Norman F.
458 GCCTGTTGAAAGATGCCGCCGTGATCAGTTGGACTAAGGATGGGGTGCACTTGGGGCCCA 517
                                                                              Score 1182.2; DB 5; Length 2469; Pred. No. 1.1e-280;
                                                      Indels
                                                      24;
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1003 AGATAGCCATTGACAGAGAGAGGCCCCGCCTGATAGCCTTTCTTAATCGCCTTTCGCCCCTTTCCCCCCCTTTCCCTTACTCCTTTATCCCCCCTTTCTTAATCGCCTTTCTTAATCGCCTTTCTTAATCGCCTTTCTTAATCGCCTTTCTTAATCGCCTTTCTTAATCGCCTTTCTCCTTACTCCTTCTTCTTCTTATCCCCCAATTTCCCCCAATTTCCCCCAATTTCCCCCAATTTCCCCCAATTTCCCCCAATTTCCCCCAATTTCCCCCAATTTCCCCCAATTTCCCCCC
 223 TTAACACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACTTTTGAGGAGG

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CCGTCTTCTCTCATGAGCCGCTGCCCGAGGAGCCCTGCCTG	CTGTTTTTTCTCCAGACCCCATGCCTTACGAACCATGCCTTCCTCAGTATCCA 2712	ACCAGTACTCCCCCAGCTTTCCCGACACCCGGAGCTCTACGTGCTCCTCAGGGGAGGATT 2380	AACAGTATTCACCTAGTTACCCTGACACAAGAAGTTCTTGTTCTTCAGGAGATGATT 2659	TGGACCGCATCGTGGCCTTGACCTCCAACCAGGAGTACCTGGACCTGTCCATGCCCCTGG 2320	TGGATTCGAATTCTCACTCTCACAACCAATGAGGAATACTTGGACCTCAGCCAACCTCTCG 2602	GGGACTGCTGGCAGTGCCCTCACAGAGACCCACCTTCAAGCAGCTGGTGGAAGACC 2260	GGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACGTTCAAGCAGTTGGTAGAAGACT 2542	AGGAGGGTCACCGCATGGACAAGCCCAGTAACTGCACCAACGAGCTGTACATGATGATGC 2200	AGGAAGGACACAGAATGGATAAGGCCAGCCAACTGCACCAACGAACTGTACATGATGATGA 2482	TCACTCTGGGCGGCTCCCCATACCCCGGTGTGCCTGTGGAGGAACTTTTCAAGCTGCTGA 2140	TCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCCGTGGAGGAACTTTTTAAGCTGCTGA 2422	ACCGGATCTACACCCACCAGAGTGATGTGTGTGTGTCTTTCGGGGTGCTCCTGTGGGAGATCT 2080	2303 ATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTCGGGGGTGTTAATGTGGGAGATCT 2362
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CORRESPICATION DATA:

APPLICATION DATA:

FILING DATE:

APPLICATION DATA:

APPLICATION WHEER: US 07/934.372

FILING DATE: 21-MIG-1992

PRIOR APPLICATION DATA:

APPLICATION WHEER: US 07/934.372

FILING DATE: 10-COT-194

PRIOR APPLICATION DATA:

APPLICATION WHEER: US 07/934.372

FILING DATE: 10-COT-194

PRIOR APPLICATION DATA:

APPLICATION WHEER: US 07/934.372

FILING DATE: 10-COT-194

PRIOR APPLICATION WHEER: US 07/934.372

FILING DATE: 01-COT-194

PRIOR APPLICATION WHEER: US 07/934.372

PRIOR APPLICATION WHEER: US 07/ MESSULT 14
US-08-451-822A-14
US-08-451-822A-14
Sequence 14, Application US/08451822A
Patent No. 585388
GENERAL INFORMATION:
APPLICANT: Diame, Craig A
APPLICANT: Cumley, Graig A
APPLICANT: Joye, Michael C
APPLIC

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Best Local :
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1343 TGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATTACAGCTTCCCCAGACTACCTGG 1402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2662 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           458 GCCTGTTGAAAGATGCCGCCGTGATCAGTTGGACTAAGGATGGGGTGCACTTGGGGCCCA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 70.8
nes 1621; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                CAGGGGAGTATACGTGCTTGGCGGGTAACTCTATCGGACTCTCCCCATCACTCTGCATGGT
                                                  CTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGGATATCCTTTCACTCTGCATGGT 1342
                                                                                           TTAATACCACCGACAAAGAGATGGAGGTGCTTCACTTAAGAAATGTCTCCTTTGAGGACG
                                                                                                              TTAACACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACTTTTGAGGACG
                                                                                                                                                                         ACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTCAAGGCCGCCGGTG 1222
                                                                                                                                                                                                                                          TCTGCAAGGTTTACAGTGATGCCCAGGCCCCACATCCAGTGGATCAAGCACGTGGAAAAGA 1162
                                                                                                                                                                                                                                                                               TCCTGCAAGCAGGGTTGCCCGCCAACAAAACAGTGGCCCCTGGGTAGCAACGTGGAGTTCA 913
                                                                                                                                                                                                                                                                                                     TCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGAGGACGTAGAGTTTG 1102
                                                                                                                                                                                                                                                                                                                                                                                                           AATTCAAACCTGACCACAGAATTGGAGGCTACAAGGTCCGTTATGCCACCTGGAGCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCGCTGCCCAGCCGGGGGGAACCCAATGCCAACCATGCGGTGGCTGAAAAACGGGAAGG 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCCCCAGAAAAGATGGAAAAGAAATTGCATGCAGTGCCGGCTGCCAAGACAGTGAAGT 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGAGGAGAAAGAAACAGATAACACCAAACCAAACCGTATGCCCGTAGCTCCATATTGGA 553
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                                                                                                                                                          ATGGGAGCAAGATTGGCCCAGACAACCTGCCTTATGTCCAGATCTTGAAGACTGCTGGAG
                                                                                                                                                                                                                                                                                                                                               ACGGCAGCATCAACCACACATACCAGCTGGATGTCGTGGAGCGGTCCCCTCACCGCCCCA
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                                                                                                                                                                                                                       TGTGTAAGGTGTACAGTGACCCGCAGCCGCACATCCAGTGGCTAAAGCACATCGAGGTGA
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70.8%;
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Pred. No. 2.9e-280;
0; Mismatches 644;
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Pred. No. 2.9
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US-08-323-430-14
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                                                                                                           ; MOLECULE TYPE: cDNA
US-08-323-430-14
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Patent No. 6344546
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 454-38
TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Crumley, Greg
APPLICANT: Jaye, Michael C
APPLICANT: Schlessinger, Joseph
TTTLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 15
                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2662 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,534
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION IMPORMATION:
TELEPHONE: (215) 454-3817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assignment of the control of
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COMPUTER READAGLE FORM.

MEDIUM TYPE: Floopy disk

COMPUTER: LIM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PSCENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
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STREET: 500 Arcola i
CITY: Collegeville
STATE: PA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Goodman, Rosanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCCCACTC 2728
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70.8%;
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    Score 1180.6; DB 4;
Pred. No. 2.9e-280;
                                            Length 2662;
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TGACCGTTCTGGAAGCCCTGGAAGAGGCCGGCAGTGATGACCTCGCCCCTGTACCTGG

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TTAACACCACGGACAAAGAGATTGAGGTTCTCTATATTCGGAATGTAACTTTTTGAGGACG 1282 ATGGGAGCAAGATTGGCCCAGACAACCTGCCTTATGTCCAGATCTTGAAGACTGCTGGAG 1033

TTAATACCACCGACAAAGAGATGGAGGTGCTTCACTTAAGAAATGTCTCCTTTGAGGACG

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TGTGTAAGGTGTACAGTGACCCGCAGCCGCACATCCAGTGGCTAAAGCACATCGAGGTGA 973 TCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAGTGGATCAAGCACGTGGAAAAGA 1162 TCCTGCAAGCAGGGTTGCCCGCCAACAAAACAGTGGCCCTGGGTAGCAACGTGGAGTTCA 913 TCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGAGGAGGACGTAGAGTTTG 1102

ACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTCAAGGTTCTCAAGGCCGGCGGGTG 1222

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AGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCCTGTATGGTGGTAACAGTCATCC 1462

1274 TCTACAAGATGAAGAGTGGTACCAAGAAGAGTGACTTCCACAGCCAGATGGCTGTGCACA 133:

923 TTATGGAAAGTGTGGTCG                  734 TAATGGACTCTGTGGTGG	863 AGTTTAAGCAGGAGCATO	803 TTCGCTGCCCAGCCGGG	743 CCAACAGAAAAGATGO	698 ATTTTGTCAGTGAGAACA	638 TGAATGTCACAGATGCCA 	578 CCGGCCTCTATGCTTGTA	518 ACAATAGGACAGTGCTTA	458 GCCTGTTGAAAGATGCCC	tches 1621; Conservative
TTATGGAAAGTGTGGTCCCCATCTGACAAGGGAAATTATACCTGTGTGGTGGAGAATGAAT	AGTTTAAGCAGGAGCATCGCATTTGGAGGCTACAAAGTRCGAAACCAGCACTGGAGGCTGCA   1   1   1   1   1   1   1   1   1   1	TTGGTTGGCAGCGGGGGAACCAATGCAACCATCGGGGGTGGTGAAAAAGGGAAC TGAAATGGCCTTCCAGTGGGACCCCAAACCACACTGCGTTGAAAAATGGCAAAG TGAAATGGCCTTCCAGTGGGACCCCAAACCCCCACACTGCGTTGAAAAATGGCAAAG	CANCACACAAAAGRIGGAAAAGCGGCTCCATGCTGTGCCTGCGCCCAACACTGTCATTCTCTCTC	698 ATTTTGTCAGTGAGAAGAGTAACAACAAGAGAGCACCATACTGGA	TGANTGTCACAGATGCCATCTCATCCGGAGATGATGAGGATGACACCGATGGTGCGGAAG 697	COGGCCTCTATGCTTGCTACTGCCAGTAGGACTGTAGACAGTGAAACGTTACTTGATGG 637	ACAATAGGACACTGCTTATTGGGGAGTACTTGCAGATAAAGGGCGCGACGCCTAGGACT 1110-11 CLAACCGCACCGCATCACAGGGAGAGGTGGAGGTGGAGGTCCGTGCCGGAGACT	GEOTETTGANAGATGECCCCCTGATCAGTTGGACTAAGGATGGGGTCCACTTGGGGCCCA 517 GEOTEGGGACGATGTGCAGACCATCAAGACATGCGCGGGGCGAAA 313	0; Mismatches
GTGGTGGAGAATGAAT                 ATTGTGGAGAATGAGT	CAGCACTGGAGCCTCA           GCCACCTGGAGCATCA	CTGAAAAACGGGAAGG 	GCCAACACTGTCAAGT                   GCCAAGACAGTGAAGT	AGAGCACCATACTGGA                 GTAGCTCCATATTGGA	ACCGATGGTGCGGAAG       ATGATGACTCCTCTT	ACTTGGTACTTCATGG		STGCACTTGGGGCCCA	644; Indels 24; Gaps
982 793	922 733	862 673	802 613	742 553	697 493	637 433	577 373	517 313	ips 3;

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407	2543 TGGATCGAATCTACCTCCACAACCAATGAGGAATACTTGGACCTCAGCCAACCTCTGG 2
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482 287	2423 AGGAAGGACAGAATGGATAAGCCAGCCAACTGCACGAACGA
422 227	2363 TOACTITAGGGGCTGCCCCTACCAGGATTCCCGTGGAGGAACTTTTTAAGCTGCTGA 2 1111   1   1   1   1   1   1   1   1
362 167	230) ATAAAGTATACACTCATCAGAGTACTGCGGTCCTTCGGGGTGCTTATTCTGGGACATCT 2 2108 ACCGGATCTACACCCACGAGTGATGTGTGGTGCTCTTTCGGGGTGCTCCTTGTGGGACATCT 2
302 107	2243 ACADANAGACCACCANTGGGGGGTTCCAGTCAAGTGGATGGTCCAGAAGCGTGTTTG 2 2048 ATANANGACAACCAACGGCCGCTGTGAAGTGGATGGCACCAGCGGGTTTTG 2 2048 ATANANGACAACCAACGGCCGCCTGTGAAGTGGATGGCACCCGAGGCATTATTTG 2
242 047	2183 ACANTGIGATGAAAATAGCAGCTTTGGACTGGCAGAGATATCAAAAATAGACTATT 2 1183 ACANTGIGATGAAAATAGCAGCTTTGGACTGGCACAGAGTATCAAAAATAGAAAAATAGCAGCTTTGGACCTGCGACGGGACATTCACCACATCGACTACT 2 1988 ACANTGIGATGAAGATAGCAGACTTTGGCCTCGCACGGGACATTCACCACCACCACCACTACT 2
182 987	213 TGGCTTCCAAAATGTATKTGATCGAGATTTAGGAGCAAATGTTTTGGAAGAAAA 2 113 TGGCTTCCCAAAATGTATKTGATCGAGAGATGTTAGGAGAGAAA 2 113 TJL
122 927	2063 AGATGACCITCAAGGACTIGGIGICATGCACCTACCAGCIGGCCAGAGGCAIGGAGIACT 2
062 867	2003 GAGCCCGGAGGCCACCCGGGATGGAGTACTCCTATGACATTAACCGTGTTCCTGAGGAGC 2
002 807	1943 ATGGGCCTCTTGTANGTCANTAGTTGAGTNAGCTGTGAAAGGCAACCTCCGAGAATACCTCC 2 1943 ATGGGCCTCTTGTANGTCANTAGTTGAGTTGAGTNCCCTCCAAAGGCAACCTGCCGGAGTACTGC 111111
942	188 TRANGARGATGANTOGGAAACACAAGARTATCATAAATCTTCTTGGACCCTGCAAACAGG 1 1181   1111   111   11   11   11   11
882	1823 AGATGITGAAAGATGATGCCACAGAGAAAGACCTTTCTGATCTGGTGTCAGAGATGGAGA 1 
822 627	1763 TRGCGGAAACCAATGGGAATGGAAAAAAAAAAACCCAAGGAGGAGCGGTGACGGTGACGGTGACAAAAAAAA
762	1703 CAAGAGATAAGCTGACACTGGGGAAGAGCCCCTGGGAGAAGTTGCTFTGGGGAAGTGGTCA 1
702	SCIGC 1
642	1583 CCATGAACTCCAACACCCGCCTGGTGAGGATTAACAACGGCCTCTCTTTCAACGGCAGACA 1 1394 CCATGAACTCTGGGGTTCTTCTGGTTCGGCCATCACGGCTCTCCTCCAGTGGGA 1
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2720 ACGGCAGTG 2728
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2528 TTGCCAATG 2536
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2608 HACAGTATTCACCTAGTTACCCGACAACAGAGTCTT--TGTTCTCTCAGGGAGAGTGTT-2659
2408 ACCAGTACTCCCCCCAGCTTTCCCCGACACCCGGAGCTCTACGTGCTCCTCAGGGGAGGATT 2467
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Search completed: December 11, 2002, 14:33:23 Job time : 144 secs

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/gqn2_6/ptcdata//pubpna/US05_RUB.seq:
/gqn2_6/ptcdata//pubpna/US06_RUB_RUB.seq:
/gqn2_6/ptcdata//pubpna/US06_RUB.yuB.seq:*
/gqn2_6/ptcdata//pubpna/US05/_RUB.yuB.seq:*
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US-10-108-605-250
US-9-814-950-3
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US-10-040-739-91
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US-09-94-456-199
US-09-95-302-271
US-09-917-8004-466
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 US-09-960-352-10423
US-09-960-352-5581
US-09-960-352-5227
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Compugen Ltd
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Sequence 91, Appl
Sequence 10423, A
Sequence 5581, Ap
Sequence 5227, Ap
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Sequence 3, Appli
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                                                                                271, App
48, Appl
146, Appl
1, Appl
1, Appl
1, Appl
182, Appl
4969, Ap
380, App
380, App
5969, Ap
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1599, Ap
271, App
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RESULT 1 US-09-954-456-293

Sequence 293,

Application US/09954456

Patent No. US20020115057A1

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159.4	159.4	159.4	159.4	159.4	159.4	166.8	169.4	171.6	171.6	177.4	177.4	179	181.6	192.8	192.8	192.8	194	203	217.2	218.4	225.4	232.6	233.6	235.6	237.6
3.7	3.7	3.7	3.7	3.7	3.7	3.9	4.0	4.0	4.0	4.2	4.2	4.2	<b>م</b> ن	4.5				8	5.1	5.1	5. 3	٥. 4	ს	5.5	5.6
6412	6378	4054	3270	3270	3270	332	3992	5084	5084	9108	4425	6827	366	5470	5406	5406	3914	379	352	395	355	391	392	402	410
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US-09-769-987-1 ALIGNMENTS	US-09-919-497-40	US-09-955-363-35	US-09-866-510-5	US-09-866-510-3	US-09-866-510-1	US-09-960-352-10875	US-09-944-807-9	US-09-967-768A-277	US-09-954-531-1383	US-09-982-610-45	US-09-982-610-31	US-09-982-610-17	US-09-960-352-10878	US-09-766-678-1	US-09-872-136-5	US-09-919-408-5	US-10-044-090-148	US-09-728-445-340	US-09-960-352-4640	US-09-867-701-3177	US-09-960-352-1177	US-09-960-352-2603	US-09-960-352-4293	US-09-960-352-14442	US-09-960-352-4303
Sequence 1, Appli	0	35,	Sequence 5, Appli	ω	Sequence 1, Appli	Sequence 10875, A	Sequence 9, Appli	Sequence 277, App	Sequence 1383, Ap	4		Sequence 17, Appl	Sequence 10878, A	Sequence 1, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 148, App	Sequence 340, App	Sequence 4640, Ap	3177,	Sequence 1177, Ap	2603	4293		Sequence 4303, Ap

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PRIOR APPLICATION NUMBER: U5/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR PRILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: U5/60/234,923
PRIOR APPLICATION NUMBER: U5/60/235,334
PRIOR APPLICATION NUMBER: U5/60/235,334
PRIOR APPLICATION NUMBER: U5/60/235,637
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: U5/60/235,638
PRIOR APPLICATION NUMBER: U5/60/235,711
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: U5/60/235,711
PRIOR FILING DATE: 2000-09-26
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                                                            SEQ ID NO 293
                                                                                                                PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER: 0F SEO ID NOS: 2276
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CURRENT FILING DATE: 2001-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Process
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
                                                                                      SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/60/233,617 PRIOR FILING DATE: 2000-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Young, Paul
TYPE: DNA
                          LENGTH: 4268
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; ORGANISM: Homo US-09-954-456-293

Query Match Best Local Similarity Matches 4268; Conserv

Conservative

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Mismatches

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Score 4268; Pred. No. 0;

DB 10; 0, Indels Length 4268; O

1080	GAGGATGGCTTCACCGGCCCATTCTTCCAAGCCGGACTGCCGCCAAATGCCTCCACAGTG [ - - - - - - - - - - - - - - - - - - -	1021	B 3
1020	CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		망
1020	ACCTGTGTGGGGGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTG	961	Qy
960			Db
960	GAAACCAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTAT	901	Q
900	-		문
900	GGTGGCTGAAAAAGGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTA	841	οy
840	CCTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGAACCCCAATGCCAACCATG	781	9
840	CTGCGGCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGAACCCAATGCCAACCATG		9
780	ACAAGAGGAGCATACTGGACCACAGAAAAGATGGAAAAGCGGCTCCATGCTTG	721	Db
780	CANGAGAGCACCATACTGGACCAACACAGAAAAGATGGAAAAGCGGCTCCATGCTGTG		οy
720	TCCGGAGATGAGGATGACACCGATGGTGCGGAAGATTTTGTCAGTGAGAACAGTAAC	661	Db
720	CCGGAGATGATGAGGATGACACCGATGGTGCGGAAGATTTTTGTCAGTGAGAACAGTAAC	661	γo
	AGTAGGACTGTAGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCA	601	Db
660	GTAGGACTGTAGACAGTGAAACTTGGTACTTCATGGTGAATGTCACAGATGCCATCTCA	601	γo
600	GAGTACTTGCAGATAAAGGGCGCCACGCCTAGAGACTCCGGGCCTCTATGCTTGTACTGCC	541	Db
600	AGTACTTGCAGATAAAGGGCGCCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCC	541	οy
540	ATCAGTTGGACTAAGGATGGGGTGCACTTGGGGCCCCAACAATAGGACAGTGCTTATTGGG	481	В
540	TCAGTTGGACTAAGGATGGGGTGCACTTGGGGCCCCAACAATAGGACAGTGCTTATTGGG	æ	δō
480	TACGTGGCTGCGCCAGGGGAGTCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCCGCCGTG	421	망
480	ACGTGGCTGCCCAGGGGAGTCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCGCCGTG	N	γo
420	GATACCACATTAGAGCCAGAAGAGCCAACCAACTACCAAATCTCTCAACCAGAAGTG	361	DЬ
420	TACCACATTAGAGCCAGAAGAGCCACCAACCAAATACCAAATCTCTCAACCAGAAGTG	361	γo
360	TCACCATGGCAACCTTGTCCCTGGCCCGGCCCTTCAGTTTAGTTGAG	301	рь
360	GGTCGTCGTCACCATGGCAACCTTGTCCCTGGCCCGGCCCTCCTTCAGTTTAGTTGAG		Ϋ́O
	AAGAGGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGC	241	망
300	ATGGAAGAGGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGC	241	γo
240	TTGCGCGTAGTCCATGCCCGTAGAGGAAGTGTGCAGATGGGATTAACGTCCACATGGAGA	181	Db
240	TGCGCGTAGTCCATGCCCGTAGAGGAAGTGTGCAGATGGGATTAACGTCCACATGGAGA	181	γ
180	AGTGACTGCAGCAGCGCGGCGCCTCGGTTCCTGAGCCCACGCCGCAGGCTGAAGGCA	121	망
180	AGTGACTGCAGCAGCAGCGGCAGCGCCTCGGTTCCTGAGCCCACCGCAGGCTGAAGGCA	121	δ
120	TCATCCGACCACGGGGGGGGGGGACAACACAGGTCGCGAAGAACGTTGCCATTC TCATCCGACCACGCGGGGGGGGGG	61	B 3
	CCAAGGACCACTCTTCTGCGTTTGGAGTTGCTCCCCAACCCCCGGGCTCGTCGCTTTC	: .	6
	CCCAAGGACCACTCTTCTGCGTTTTGGAGTTGCTCCCCACAACCCCGGGCTCGTCGTCGTTTC		3 3

2220	AGAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGACTTTGGACTCGCCAGA	2161	Qy
2160	CTGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGAGTTTAGCAGCC	2101	. Db
2160	TGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAG	2101	Qy
2100	TTCCTGAGGAGCAGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAG	2041	· pb
2100	AACCGTGTTCCTGAGGAGGAGGATGACCTTCAAGGACTTGGTGTCATGCACCTACCAG	2041	Оу
2040	GGCAACCTCCGAGAATACCTCCGAGCCCGGGAGGCCACCCGGGATGGAGTACTCCTATGAC	1981	Db
2040	GCAACCTCCGAGAATACCTCCGAGCCCGGAGGCCACCCGGGATGGAGTACTCCTAT	1981	Qy
1980	CTTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAA	1921	Db
1980	TTCTTGGAGCCTGCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAA	9	Qy
1920	GATCTGGTGTCAGAGATGGAGATGAATGATGATGATGGGAAACACAAGAATATCATAAAT	1861	DЬ
1920	ATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGAAACACAAGAATATCATAAAT	æ	Оу
1860	GAGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAAGACCTTTCT	1801	Db
1860	AGGCGGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACCTTTCT	1801	Qy
0081		1741	Db
1800	GTTGCTTTGGGCAAGTGGTCATGGCGGAAGCAGTGGGAATTGACAAAGACAAGCCCCAAG	1741	γQ
1740	GAGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCCTGGGAGAA	1681	Db
1740	AGGACCCAAAATGGGAGTTTCCAAGAGATAAGCTGACACTGGGCAAGCCCCCTGGGAGAA	1681	Qy
1680	CGCCTCTCTTCAACGGCAGACACCCCCCATGCTGGCAGGGGGTCTCCGAGTATGAACTTCCA	1621	Db
1680	GCCTCTCTCAACGGCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCA		Qy
1620	GTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA	1561	Db
1620	TTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACA	1561	ОУ
1560	AGCAGCCAGCCGGCTGTGCACAAAGCTGACCAAACGTATCCCCCCTGCGGAGACAGGTAACA	1501	Db
1560	GCAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAACA	1501	γo
1500	TGTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTC	1441	Db
1500	GTATGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTC	4	οy
1440	ACAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCC	1381	DЬ
1440	CAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCC	1381	δ
1380	ATATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATT	1321	Db
1380	TATCCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATT	1321	γQ
1320	CGGANTGTAACTTTTGAGGACGCTGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGG	1261	Db
1320	GGAATGTAACTTTTGAGGACGCTGGGGGAATATACGTGCTTGGCGGGTAATTCTATTGGG	1261	Qy
1260	AAGGTTCTCAAGGCCGCCGGTGTTAACACCCACGGACAAAGAGATTGAGGTTCTCTATATT	N	Db
1260	STTCTCAAGGCCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTCTATATT	1201	οy
1200	TGGATCAACCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTC	1141	Db
1200	GGATCAAGCACGTGGAAAAGAACGGCAGTAAATACGGGCCCGACGGGCTGCCCTACCTC	1141	Qy
1140	AGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGGCCCCACATCCAG	1081	DЬ
1140	CGGAGGAGACGTAGAGTTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCCACATCCAG	1081	Qy

3300	TTTTAATAGCTATTTGCTAAATGCTGTTCTTGCACATAATTTCTTAATTTTCACCGAGCA	3241	Qy
3240	ATTTTTTGTATTGATTTTAAATGGATGTCCCAATGCACCTAGAAAATTGGTCTCTCTT	3181	Db
3240	TTTTTGTATTGAATTTAAATGGATGTCCCAATGCACCTAGAAAATTGGTCTCTCT	3181	Qγ
3180	TGGATGTANGTANATATATCANATTATGTATANATATATATATATATATATATATAGGAGT TGGATGTATGT	3121	₽ <i>Q</i> y
3120	NATTGGAGAGATTTATGTCAGCACACACTTACAGAGCACAAATGCAGTATATAGGTG	0	뮹
3120	— ຄ	3061	Qy
3060	CCTGTGGACCAGTAGGACTCAAGGTGGACGTGCGTTCTGCCTTCCTT	3001	рb
3060	CTGTGGACCAGTAGGACTCAAGGTGGACGTGCGTTCTGCCTTCCTT	3001	VΩ
0	TCTGGAGCAGTGGACTGCCACAAGCCACCATGTAACCCCTCTCACCTGCCGTGCGTTCTG	2941	В
3000	CTGGAGCAGTGGACTGCCACAAGCCACCATGTAACCCCTCTCACCTGCCGTGCGTTCT	2941	Qy
2940	TATGTGTAAAGATTTATACAGTTGAAAACTTGTAATCTTCCCCAGGAGGAGAAGAAGGTT	2881	Db
2940	ATGTGTAAAGATTTATACAGTTGAAAACTTGTAATCTTCCCCAGGAGGAGGAAGAAGGT	2881	οy
2880	TTGTTGTCTCCACTTGTATATATGGATCAGAGGAGTAAATAATTGGAAAAGTAATCAGCA	2821	В
2880	TGTTGTCTCCACTTGTATATATGGATCAGAGGAGTAAATAATTGGAAAAGTAATCAGC	2821	Ωy
2820	CANACAGGACACTGGGAACCTAGCTACACTGAGCAGGGAGACCATGCCTCCCAGAGC	2761	Db
2820	AAACAGGACAGCACTGGGAACCTAGCTACACTGAGCAGGGAGACCATGCCTCCCAGAG	2761	Qγ
76		7	뮹
76	CTCAGTATCCACACATAAACGGCAGTGTTAAAACATGAATGA	7	γo
70	IGTTCTTCAGGAGATGATTCTGTTTTTCTCCAGACCCCATGCCTTACGAACCATGCCTT	2641	₽
2700	GTTCTTCAGGAGATGATTCTGTTTTTTCTCCAGACCCCATGCCTTACGAACCATGCCT	2641	δ
6	CTCAGCC	2581	망
2640	TGGACCTCAGCCAACCTCTCGAACAGTATTCACCTAGTTACCCTGACACAAGAAGTTC	2581	δō
50	TCAAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCTCACAACCAATGAGGAATAC	2521	Ð
2580	TCAAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCTCACAACCAATGAGGAAT	2521	γo
2520	AACGAACTGTACATGATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCCAGAGACCCAACG	2461	DЬ
2520	ACGAACTGTACATGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAAC	2461	οy
2460	GAGGAACTTTTTAAGCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCC	2401	B
2460	AGGAACTTTTTAAGCTGCTGAAGGAAGGACACAGAATGGATAAGCCAGCC	2401	у
2400	GGGCTCTTAATGTGGGAGATCTTCACTTTAGGGGGCTCGCCCTACCCAGGGATTCCCCTG	2341	Db
2400	GGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGGCTCGCCCTACCCAGGGATTCCCCT	2341	Qγ
2340	CTCCAGAA	N I	문 5
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2280	GATATCAACAATATAGACTATTAGAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGG	2221	문 5
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2220		2161	Db

	AAAAAAA 4268   AAAAAAAA 4268   AAAAAAAA 4268	4261	pb 04
4260 4260	ncagatattaatgttaacaagacaaaataaatgtcacgcaacttaaaaaaa 		Оy
4200 4200	TGTTACAAAATTGGAGAAGTATTTAATAAAACCTGTTAATTTTTATACTGACAATAAAA 		рь
4140 4140	AAAAACCCAGTCACTTTGCAATAGCGGTGCAAGATGAATGCAGATTACACTGATCTTTATG AAACACCCAGTCACTTTGCAATAGCGGTGCAAGATGAATGCAGATTACACTGATCTTATG	4081	Дb
4080	TACATCAGACAAAATATGGCGGTTGTTCGTCTGTGTACTAAAGTATTGTGTTTTGGTTTGG 	4021	Оу
4020 4020	TAAAGGATTGCTTTAATCTAATCTGGCAGGACCTCACCAAAAGTCAGGCCTCATCACTTAAGGTTTAATCTGGCAGGACCTCACCAAAAGATCAGGCCTCATCACTTAATCTGGCAGGACCTCACCAAAAGATCCAGCCTCATAGC	3961 3961	Qу
3960 3960	TCATAGAAAATGAACACAGGTGTTCTGCTCATAGGTTTGGGGATACGTCCATCTTTT	3901	Db 04
3900 3900	TTIGATAATGGCTTCCAGACTCTTTGGGTTGGAGACGCCTGTTAGGATCTTCAATGTCAATGTCAATTCAATAATGGCTTCCAGACTCTTTGGGTTGGAGACGCCTGTTAGGATCTCTAAGGTCTCCAAGTCCCCA	3841	Db
3840 3840	GCTGGCCTTCTGCTTCTGAGTTGGACATTAATCAGATTAGCCTGATTCTCTTCAGTGAATT	·3781 3781	ру
3780 3780	ATCCATTCCTTGAGGACACACCTTAGTTGAAATGATAGCAGAATGTGCTCTCTCT	3721 3721	D Qy
3720 3720	CANCETCHACTGGACTTCCCAAGATAATGGTACCAGGCCCCCTTAAAAGATGCCTTACTGACTTCCCAAGATAAATGGTACCAGGCTCCTCTTAAAAGATGCCTTACTGCCAAGATAAATGGTACCAGGGTCCTCTTAAAAGATGCCTTA	3661 3661	pg Qy
3660 3660	AGRACTCATTCATAGGAAGGTGTTTCATTTTGGTGTGCAACCCTGTCATTAGGTCAACG AAGAACTCATTCATAGGAAGGTGTTTCATTTTGGTGTGCAACCCCTGTCATTAGGTCAACG AAGAACTCATTCATAGGAAGGTGTTTCATTTTGGTGTGCAACCCCTGTCATTAGGTCAACG	3601	pb oy
3600 3600	ATGCTGCTGTCAGACGATTGTTCTTAGACCTCCTAAATGCCCCATATTAA 		D Q
3540 3540	TTGAAAAGAGAATATTTACAATATATGACTAATTTGGGGAAATGAAGTTTTGATTTAT	3481 3481	Оу
3480 3480	ATGCAGCAGCAGACAGCAGACTAGTTAATCTATTGCTTGGACTTAACTAGTTATCAGATCC	3421 3421	Db Qy
3420 3420	TGGTAATATACAAAACAATTAATCATTTATAGTITTTTTTGTAATTTAAGTGGCATTTCT	3361 3361	Db Qy
3360	GAGGTGGAAAAATACTTTTGCTTTCAGGGAAATGGTATAACGTTAATTTATTAATAAAT	3301	B 8
30	TTTAATAGCTATTTGCTAAATGCTGTTCTTACACATAATTTCTTAATTTTCACCGAGCA	24	₽

RESULT 2 US-09-954-456-1599

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; NAME/KEY: misc_feature
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SOFTWARE: Patentin versic
SEQ ID NO 1599
LENGTH: 4258
TYPE: DNA
ONGANISM: Homo sapiens
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PRICE APPLICATION NUMBER: U5/60/234, 057

PRICE THE CONTROL OF 
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Best Local Similarity
Matches 4268; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Sets
                                                                     361
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                                                                                                                                                       301
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                    421 TACCTGCCTGCCCAGGGGAGTCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCGCCGTG
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1500	TGTATIGGTGGTAACAGTCATCCTGTGCGGAATGAAGAACAGGACCAAGAAGCCAGACTTC TGTATIGGTGGTAACAGTCATCCTGTGCGGAATGAAGAACAGGACCAAGAAGCCAGACTTC	1441
4	CAGCTTCCCCAGACTACCTGGAGATAGCCATTACTGCATAGGGGTCTTCTTAATCGC	1381
44	CAGCTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGC	w
1380	ATRICCTTTCACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATT	1321 1321
1320 1320	GGAATATACGTGCTTGGCGGGTAATTCT 	1261 1261
6 6	GCCGCCGGTGTTAACACCACGGACAAAGAGATTGAGGTTCTC 	NN
1200 1200	AGAACGGCAGTAAATACGGGGCC              AGAACGGCAGTAAATACGGGCCC	1141 1141
1140 1140	TTTGTCTGCAAGGTTTACAGTGATGCCCAGCCCC 	1081
1080	GCCTCACCGGCCCATCCTCCAAGCCGGACTG 	1021
1020	TGGTGGAGAATGAATACGGGTCCATCAATCA 	961 961
960	TGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAAT 	901
900	CTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTA 	841 841
B40 B40	AGTTTCGCTGCCCAGCCGGGGGGAACCCAATG 	781 781
780 780	ACCAACACAGAAAAGATGGAAAAGCG 	721 721
720 720	GACACCGATGGTGCGGAAGATTT 	661
099	actgtagacagtgaaacttggtacttcatggtgaatgtcacagat 	601
600	CAGATAAAGGGCGCCACGCCTAGA 	541 541
540	ATGGGGTGCACTTGGGGCCCAACAATAGGACAGTGC 	481 481
480	TACGTGGCTGCGCCAGGGGAGTCGCTAGAGGTGCGCTGCCTGTTGAAAGATGCCGCCGTG	421

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2640 2640	TIGGACCTCAGCCAACCTCTCGAACAGTATTCACCTAGTTACCCTGACACAGAAGTTTCTTTGGACCTAGCCACCAGAAGTTCTTTTTGGACCTAGCACAACAAGTTCTTTTGGACCTAGCACAACAACATCTTCTTTGGACCTAGCAACAACAAGTTCTTTTGGACCTCAGCAACAACAAGTTCTTTTTTGAACCTTAGCACCAACAACAAGTTCTTTTTTTT	2581 2581	B 8
2580 2580	TECANGEAGTTGGTACAAGACTTGGATCGAATTCTACACTCTGACAACCAATGAGGAATACC IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ശ്ശ	B 8
2520 2520	ANCGANCISTACATIGATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAGGAGCCCGCGGGGGGGG	2461 2461	B 04
2460 2460	GAGGAACTTTTTAAGCTGCTGAAGGAAGGACXACAAATGGATAAGCCAGCCAACTGCAC   III	44	B 3
2400	GGGSTGTTNAFGTGGGAGATCTTCACTTTAGGGGCTCGCCCTACCCAGGGATTCCCGTG 	2341	B 8
2340 2340	TGCTTCCAGAAGCCCTGTTTGATAGAGTATAGACTCAGTCAG	28	B 8
2280 2280	HITTELACIATETTAGACTETTECHAAAGACCACCAATGGGGGCTTCCAGTCAGTGAGTGAGTGA	N N	B 6
	GAANTGTTTTGGTAACAGAAACANGTGATGAAATMGCAGACTTTGGACTGGCGAGA 	2161	B 8
2160 2160	TGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCA 	10	B 8
2100	CGTGTTCCTGAGG            CGTGTTCCTGAGG	0 0	B 3
2040	AACCTCCGAGAATACCTCCGAGCC	8 8	B 9
1980	TRETTGGAGCETGGACACAGGATGGGCCTCTETATGTCATAGTTAGGTATGCCTTCTAGTAGGTATGCCTTCTAGTTAGT	92	D 97
1920 1920	ATCTGGTGTCAGAGATGGAGATGATGAAGATGATTGGGAAACACAAGAATATCATAAAT 		B 8
1860 1860	AGGCGTCACCGTGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACCTTTCT 	80	DF 63
1800	TTGCTTTGGGCAAGTGGTCATGGCGGAGCAGTGGGAATTGACAAAGACAAGCCCAAG 	1741 1741	Оb
1740 1740	CCAAGAGATAAGCTGACACTGGGCAAGCCCCTGGGAGAA 	1681	B 94
1680 1680	CGCCTCTTTCAACGCAGACACCCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCA	1621 1621	Db Oy
1620 1620	GTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAAAACCCCCGCTGGTGAGGATAGCAACACGCTGGTGAGGATAGCAACACGCTGGTGAGGATAGCAACACGCTGGTGAGGATAACAACACGCTGGTGAGGATAACAACACACGCTGGTGAGGATAACAACA	1561 1561	B 9
1560	GCAGCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAACA	.50	문

CANCGTCTANTGGACTTCCCAAGATAAATGGTACCAGGGTCCTCTTAAAAGATGCCTTA 3720	Qy 3661 Db 3661	
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TEGROTITAANGETGETGTCAGAGGATTGTTTAGACCTCCTAANGCCCCATATTAA 3600	ωω	
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TATTITTTGTATTGATTTAAATGGATGTCCCAATGCACCTAGAAAATGGGTCTCTTT 3240	31	
. TGGATGTATGTAAATATATTCAAATTATGTATAAATATATAT	31	
TANTTGGAGAAAATTTATGTCAGCACACACTTACAGAGCACAATGCAGTATATAGGTGC 3120	30	
GCTGTGGACCAGTAGGACTCAAGGTGGACGTGCGTTCTGCCTTGCTTAATTTTGTAA 3060	30	
TCTGGAGCAGTGGACTGCCACAAGCCACCATGTAACCCCTCTCACCTGCCGTGGGTTCTG 3000	Qy 2941 Db 2941	
TAUGUGAAAGATTTATAACAGTIGAAAACTTGTAATGCTTCCCCAGGAGGAGAAGAAGAGTT 2940 	2 2	
TTGTTGTCTCCACTTGTATATATGGATCAGAGGAGTH	Qy 2821 Db 2821	
CAAACAGGACAGGACTGGGAACCTAGCTACACTGAGCAGGAGACCATGCCTCCCAGAGC 2820	N N	
CCTCACTANTCCACACATAAACGCCAGTGTTAAAAAATGAATGAATGGCTGTGCTGCCCTCGCC 2760	Qy 2701 Db 2701	
TGTTCTTCAGGAGATGATTCTGTTTTTTGTCCAGACCCCATGCCTTACGAACCATGCCTT 2700		

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PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOPTMARE: Patentin Ver: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 271, Application US/09925302
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO4
             OTHER INFORMATION: n equals NAME/KEY: misc feature
                                             NAME/KEY: misc feature LOCATION: (3664)
                                                                             LOCATION: (3523)
OTHER INFORMATION: n equals
                                                                                                               OTHER INFORMATION: n equals NAME/KEY: misc feature
                                                                                                                                             NAME/KEY: misc feature LOCATION: (2586)
                                                                                                                                                                               ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                 TYPE: DNA
LOCATION: (3687
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                  TCCCAGAGACCAACGTTCAAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCTCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OLGA BADDMAN
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN
FILE REFERENCE: PA-028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILENG DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 48
LENGTH: 13454
TYPE: DNA
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure LOCATION: 2, 9, 16, 39, 42, OTHER INFORMATION: a, t, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Incyte ID No. US20020137081A1 493848CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2230
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                 GGAGACGTAGAGTTTGCTCTGCAAGGTTTACAGTGATGCCCAGCCCCCACATCCAGTGGATC
                                                                                   TCGCCTCACCGGCCCATCCTCCAAGCCGGACTGCCGGCAAATGCCTCCACAGTGGTCGGA 1086
                                                                                                                                                         GTGGTGGAGAATGAATACGGGTCCATCAATCACACGTACCACCTGGATGTTGTGGAGCGA 1024
                                                                                                                                                                                                          GCCACCTGGAGCATCATAATGGACTCTGTGGTGCCCTCTGACAAGGGCAACTACACCTGC
                                                                                                                                                                                                                                                                               TTGAAAAATGGCAAAGAATTCAAACCTGACCACAGAATTGGAGGCTACAAGGTCCGTTAT
                                                                                                                                                                                                                                                                                                  CTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCATTGGAGGCTACAAGGTACGAAAC
                                                                                                                                                                                                                                                                                                                                                                         GCCAACACTGTCAAGTTTCGCTGCCCAGCCGGGGGGAACCCAATGCCCAACCATGCGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                       AGAGCACCATACTGGACCAACACAGAAAAGATGGAAAAGCGGCTCCATGCTGTGCCTGCG 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCGAGGAGCCCTGCCTGCCCCGACACCCAGCCCAGCTTGCCAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACACAAGAAGTTCT---TGTTCTTCAGGAGATGATTCTGTTTTTTCTCCAGACCCCATG 2682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCAACCAGGAGTACCTGGACCTGTCCATGCCCCTGGACCAGTACTCCCCCAGCTTTCCC
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AGCAACGTGGAGTTCATGTGTAAGGTGTACAGTGACCCGCAGCCGCACATCCAGTGGCTA
                                                                 TCCCCTCACCGGCCCATCCTGCAAGCAGGGTTGCCCGCCAACAAAACAGTGGCCCTGGGT
                                                                                                                                        ATTGTGGAGAATGAGTACGGCAGCATCAACCACACATACCAGCTGGATGTCGTGGAGCGG
                                                                                                                                                                                                                                            CAGCACTGGAGCCTCATTATGGAAAGTGTGGTCCCATCTGACAAGGGAAATTATACCTGT 966
                                                                                                                                                                                                                                                                                                                                                   GCCAAGACAGTGAAGTTCAAATGCCCTTCCAGTGGGACCCCAAAACCCCACACTGCGCTGG
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72.4%;
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g, or other
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Pred. No. 5.4e-252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 561;
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2226 1797	GTTTTGGTANCAGAAAACAATGTGATGAAAATAGCAGACTTTGGACTGGCGAGAGATATC GTTTTGGTANCAGAAACAATGTGATGAAAATAGCAGACTTTGGACTGGCGAGAGATATC GTCCTGGTGACAGAGAGACAATGTGATGAAGATGAAGATGATGAGAGATT	2167 1738
2166 1737	AGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATGGAGATTTAGCAGCCAGAAAT	2107 1678
2106 1677	CONGREGORIAGAGAGAGAGACTECAAGGACTTGTTGTTGTATGCACCTACCAGCTGGCC  CONGREGORIAGAGAGAGAGACCTECCAAGGACTTGTTGTCTTGCACCTACCAGTGGCC  CACAACCCAGAGGACCAGTCCTCCCAAGGACTTGTGTCTTGCCTACCAGTGGCC	2047 1618
2046 1617	CTCCGGAATACCTCCGAGCCCCGGAGCCACCCGGAGTGGAGTACTCTATGACATTAAC	1987 1558
1986 1557	GGACCTTCCANANGANTGGCCCTCTCTATGTCATAGTTGATTAGTTGATTAGCCTTAAAGGCAAC GGACCTTCCANANGANTGGCCCTCTTTTATGTCATGTTGATTTGCTTTATGCCTTCAAAGGCAAC	1927 1498
1926 1497	GTOTOGAGATIGAGGAGAACATGATTCATTGGGAAACACAAAAATATCATTAAATCTTCTT	1867 1438
1866 1437	GTCACCOTGGCCGTGAAGATGTTCAAAGATGCCACAGAGAAAGACCTTTCTGATCTG	1807 1378
1806 1377	TTTGGCCAGTGGTCATGGCGAAGAGTGGAATTGAAAAACAAGCCAAGGCGAAGGGGGGGG	1747 1318
1746 1317	CCANATOGOROTTECANGACATANACETRACATEGOCANGCCCCTGGGACAGGETTGC	1687 1258
1686 1257	TCTTCAACGGCAGACACCCCATGCTGGCAGGGGTCTCCGAGTATGAACTTCCAGAGAC	1627 1201
1626 1200	GETGAGTCCAGETCCTGCATGAATTCTGAACACCCCGGTTGTGAGGATAACAACACGCCTC	1567 1144
1566 1143	CAGCCGGTGTGCACAAGCTAACCAAACGTATCCCCCTCGGCAACACGTAACAGTTTCG	1507
1506 1083	GTGGTAAAAGGCATCATCGTGGGCGAATGAAGAACACGACCAAAAAGCCAGACTTCAGACAGC 	1447
1446 1023	TCCCCAGACTACTGCAGATAGCCATTTACTCCATAGGGGTCTTCTTAATCGCCTGTATG	1387 964
1386 963	TTTGACTCTGCATGGTTGACAGTTCTGCCAGCGCCTGGAAGAGAAAAGGAGATACAGCT	1327
1326 903	GTAACTTTGAGACCCCGGGGATATACGGCCTGGCCGGTAATTCTATTGGGATATCC	1267 844
1266 843	CTANGECCCCCCGTCTTANACCACCGACAAAGGGTTGAGGTTCTCTATATTCGGAAT	1207 784
1206 783	AAGCACGTGGAAAAAGAACGGCAGTAAATACGGGCCCGACGGGCCTGCCCTACGCTCTCAAGGTT	1147 724

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2278 GGACACCCAGCCCAGCTTGCCAATG 2302

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US-09-917-800A-1466
SEQUENCE 1465, Application US/09917800A
Patent No. US2002019462A1
GENERAL INFORMATION;
APPLICANT: Mondrick, Donna
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Elsaboff, Michael
APPLICANT: Elsaboff, Michael
APPLICANT: Elsaboff, Michael
APPLICANT: Elsaboff, Michael
APPLICANT: Mondrie, Wolcoller Toxicology Modeling
FILE REFERENCE: 44921-5038-US
GURRENT PELLAG DATE: 2001-07-31
CURRENT PELLAG DATE: 2001-07-31
CURRENT PELLAG DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,045
PRIOR FILING DATE: 2001-05-12
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-12
PRIOR APPLICATION NUMBER: US 60/290,45
PRIOR FILING DATE: 2001-05-12
PRIOR APPLICATION NUMBER: US 60/297,336
PRIOR FILING DATE: 2001-05-13
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/299,894
PRIOR FILING DATE: 2001-05-13
PRIOR APPLICATION NUMBER: US 60/299,894
PRIOR FILING DATE: 2001-05-19
PRIOR APPLICATION NUMBER: US 60/299,894
PRIOR FILING DATE: 2001-05-19
PRIOR APPLICATION NUMBER: US 60/299,894
PRIOR FILING DATE: 2001-05-19
PRIOR APPLICATION NUMBER: US 60/299,894
PRIOR FILING DATE: 2001-05-19
PRIOR APPLICATION NUMBER: US 60/299,459
PRIOR FILING DATE: 2001-05-19
PRIOR APPLICATION NUMBER: US 60/299,459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rattus norvegicus FEATURE:
OTHER INFORMATION: Genbank
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TYPE: DNA
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TCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGGTCTCCGAGTATGAACTTCCAGAGG
                                                                                                                                    GCCAGCCGGCTGTGCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAACAGTTT 156-
                                                                                                                                                                                                       TGGTGGTAACAGTCATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTCAGCA 150
                                                                                                                                                                                                                                                                               CTTCCCCAGACTACCTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCCTGTA 144
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                                                CAGCTGACTCTAGTGCATCCATGAACTCTGGGGTTCACCTGGTTTAGCCTTCATAA----
                                                                     CGGCTGAGTCCAGCTCCATGAACTCCAACACCCCGCTGGTGAGGATAACAACACGCC
                                                                                                                 GCCAGATGGCTGTGCATAAACTGGCTAAGAGCACCCTTCTGTGCAGACAGGTAACAGTGT
                                                                                                                                                                                  TGCTGGGGTCCGTCGTCATCTACAAGATGAAAAGCGGCATCAAGAAGAGCGACTTCCATA
                                                                                                                                                                                                                                                   CCTCACCTCTGTACCTGGAAATCATTATCTATTGCACCGGGGCCTTCCTGATCTCCTGTA
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Pred. No. 8.4e-144;
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Sequence 1, Application US/09814950

PRIGHT INFORMATION:
GENERAL INFORMATION:
APPLICANT: WEI, MING HUI et al
APPLICANT: WEI, MING HUI et al
APPLICANT: WEI, MING HUI et al
TITLE OF INVENTION: NUCLEIC ACID MOLECULES EN
TITLE OF INVENTION: NUCLEIC ACID MOLECULES EN
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOOL174
CURRENY MEPLICATION NUMBER: US/09/814,950
CURRENY MEPLICATION NUMBER: US/09/814,950
CURRENY MELONG DATE: 2001-03-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
                                                                                                                                                                                                                                                                            Matches 643;
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 848
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2105
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                                                                                                                                                                                                                                                                                               Local Similarity
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CCGTAACCATGGTCAGCTGGGGTCGTTTCATCTGCCTGGTCGTCGTCACCATGGCAACCT
                                   GCCTCGGTTCCTGAGCCCACCGCAGGCTGAAGGCATTGCCGCGTAGTCCATGCCCGTAGAG
                                                                                                                                                                                                                                 GGGACAACACAGGTCGCGGAGGAGCGTTGCCATTCAAGTGACTGCAGCAGCAGCGGCAGC
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                                                                                                                                                                                              GGGACAACACAGGTCGCGGAGGAGCGTTGCCATTCAAGTGACTGCAGCAGCAGCGGCAGC 61
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                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                          15.1%; Score 643; DB 10; 100.0%; Pred. No. 1.8e-139
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                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                             Length 848
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; LOCATION: (40)..(2124)
US-09-728-952-82
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SEQ ID NO 82
LENGTH: 2184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: Tang, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 82, Application US/09728952
Patent No. US20020111302A1
                                                                                                                                                   Ouery Match 15.0%; Score 640.6; DB 10; Length 2184; Best Local Similarity 73.3%; Pred. No. 1e-138; Matches 836; Conservative 0; Mismatches 299; Indels 6;
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ujwal, Manusha L.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020111302Alel Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REPERSENCE: 799
CURRENT APPLICATION NUMBER: US/09/728,952
CURRENT APPLICATION NUMBER: US/09/728,952
CURRENT PILLIG DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 101
SOFTMARE: OF SEQ ID NOS: 101
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                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
1023 CGCAAGGCTGTCCTCA-----GGGGAGGCCCCACGCTGGCCAATGTCTCCGAGGTCGA 1076
                                                                                           1554 GGTAACAGTTTCGGCTGAGTCCAGCTCCTCCATGAACTCCAACACCCCGCTGGTGAGGAT 1613
                                     1614 AACAACACGCCTCTCTTCAACGGCAGACACCCCCATGCTGGCAGGGGGTCTCCGAGTATGA 1673
                                                                             963
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362 TAGAGGTCCCCTCCTGTTGAAAGATCCCCCCCCTGATCACTTTGGACTAAGGATGGGGTGC 421
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TGTCCCTGGCCGGCCTCCTTCAGTTTAGTTGAGGATACCACATTAGAGCCAGAAGAGC
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                                                                           GCTCAAGGTGTCCCTGGAGTCCAACGCGTCCATGAGCTCCAACACACCACTGGTGCGCAT 1022
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Wang, Jian-Rui
Wang, Junrui
Yemazaki, Vicki
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97 A 209	N I
594 A 2694	Оу 26
	Db 20
34 AAGTTCTTGTTCTTCAGGAGATGATTCTGTTTTTTTCTCCAGACCCC	Qу 26
)77 CGAGTACCTGGACCTGTCGGCGCCTTTCGAGCAGTACTCCCCGGGTGGCCAGGACACCCC 2036	Db 19
74	Qy 25
317 GCCCACCTTCAAGCAGCTGGTGGAGGACCTGGACCGTGTCCTTACCGTGACGTCCACCGA 1976	Db 19
14 ACCAACGTTCAAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTCTCACAACCAATG	Qy 25
357 CTGCACACGACCTGTACATGATGCGGGAGTGCTGGCATGCCGCGCCCTCCCAGAG 1916	Db 18
54 CTGCACCAACGAACTGTACATGATGAGGGACTGTTGGCATGCAGTGCCCTCCCAG	Qy 24
97 CCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACCGCATGGACAAGCCCGCCAA 1856	Db 17
94 TC	Qу 23
37 GTCCTTTGGGGTCCTGCTCTGGGAGATCTTCACGCTGGGGGGGCTCCCCCGTACCC	Db 17
34 GTCCTTCGGGGTGTTAATGTGGGAGATCTTCACTTTAGGGGGGCTCGCCCTACCCAGG	Оу 23
577 GAAGTGGATGGCGCCTGAGGCCTTGTTTGACCGAGTCTACACTCACCAGAGTGACGTCTG 1736	Db 16
TGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCA	Qy 22
17 GGCCCGGGACGTGCACAACCTCGACTACAAGAAGACAACCAAC	Db 16
14 CGCCAGAGATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCGGCTTCC	Qy 22
57 GGCTGCCCGCAATGTGCTGGTGACCGACGACACGTGATGAAGATCGCAGACTTCGGGC	pb 15
54 AGCAGCCAGAAATGTTTTGGTAACAGAAAACAATGTGATGAAAATAGCAGACTTTGGA	Qy 21
97 CTACCAGGTGCCCGGGGCATGGAGTACTTGGCCTCCCAGAAGTGCATCCACAGGGACCT 155	14
TACCAGCTGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATT	0у 20
	Db 14
34 CTATGACATTAACCGTGTTCCTGAGGAGC	Оу 20
377 GGCCAAGGGTAACCTGCGGGAGTTTCTGCGGGGGGGGGG	Db 13
74 CT	Оу 19
	13
14 C	Оу 19
157 CCTGTCGGACCTGGTGTCTGAGATGAGATGATGAAGATGATCGGGAAACACAAAAACAT 1316	Db 12
54 C	0у 18
.97 GGCCGCCAAGCCTGTCACCGTAGCCGTGAAGATGCTGAAAGACGATGCCACTGACAAGGA 1256	Db 11
94	Qy 17
37 TGGGGAGGGCTGCTTCGGCCAGGTGGTCATGGCGGAGGCCATCGGCATTGACAAGGACCG 1196	Db 11
34	Qy 17
77 GCTGCCTGCCGACCCCAAATGGGAGCTGTCTCGGGCCCGGCTGACCCTGGGCAAGCCCC	Db 10
74	Оу 16

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APPLICANT: Aglate real A.

APPLICANT: JORES ROBERT

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE

TITLE OF INVENTION: LAND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT SILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOPTMARE: FRATSEQ for Windows Version 4.0

SEQ ID NO 4969

LENGTH: 5144
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; ORGANISM: Homo sapien
US-09-867-701-4969
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                                                                                      Sequence 380, Application US/09895828 Patent No. US20020099012A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. US20020132237A1 GENERAL INFORMATION:
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                                   APPLICANT: Wang,
APPLICANT: McNei
APPLICANT: Watan
  APPLICANT:
                    APPLICANT:
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                                                                                                                                                                                                                                       CGTTAATTTAATAAAATTGGTAATATACAAAA 3375
                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATATATTTACAAGGAGTTATTTTTGTATTGATTTTAAATGGATGTCCCAATGCACCT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTATATATTTACAAGGAGTTATTTTTTGTATTGATTTTAAATGGATGTCCCAATGCACCT 3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATGCAGTATATAGGTGCTGGATGTATAGTAAATATTCAAATTTATGTATAAATATATA 316J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCTTGTTAATTTTGTAATAATTGGAGAAGATTTATGTCAGCACACCTTPACAAGCC 3101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCACCTGCCGTGCGTTCTGGCTGTGGACCAGTAGGACTCAAGGTGAACGTGCGTTCTGCC 304
TCACCTGCCGTGCGTACTGGCTGTGGACCAGTAGGACTCAAGGTGGACGTGCGTTCTGCC 335
                                                                                                                                                                                                                CGTTAATTAATTAATAAATTGGTAATATACAAAA 1
                                                                                                                                                                                                                                                                                                                           TCTTAATTTTCACCGAGCAGAGGTGGAAAAATACTTTTGCTTTCAGGGAAAATGGTATAA 334
                                                                                                                                                                                                                                                                                                                                                                                 AGAAAATTGGTCTCTTTTTTTAATAGCTATTTGCTAAATGCTGTTCTTACACATAATT 3281
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                                                                                                                                                                                                                                                                                        TCTTAATTTTCACCGAGCAGGTGGAAAAATACTTTTGCTTTCAGGGAAAATGGTATAA
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          McNeill, Patricia D
Watanabe, Yoshihiro
Carter, Darrick
Henderson, Robert A.
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                                                                    Tongtong
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Pred. No. 4.2e-107;
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                                                                                                                                                                                                                                                                                  US-09-867-701-9869/c
                    APPLICANT: AGIACO, PAUL A.
APPLICANT: JORES MODERT
APPLICANT: HATLOCKET, SUSSAI I.
TITLE OF INVENTION: AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIGMOSIS OF OVARIAN CANCER
FILE REFERENCE: 21012, 497
CURRENT PAPLICATION INVEST: US/09/867,701
CURRENT PAPLICATION INVEST: US/09/867,701
SUMBER OF 500 ID MOS: 10912
SUPPLARE: PARKSON FOR MINDOWS VERSION 4.0
SECURIOR SESSON FOR MINDOWS VERSION 4.0
SECURIOR OF MINDOWS VERSION 4.0
                                                                                                                                                                                                                             Sequence 9869, Application Patent No. US20020132237A1 GENERAL INFORMATION:
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LENGTH: 446

US/09867701

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; OTHER INFORMATION: n = US-09-895-828-380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KAIOS, MICHAEL D.
TITLE OF INVENTION: CAMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DAGNOSIS OF LUNG CANCER
FILE REFERENCE: 21012; 359
CURRENT APPLICATION NUMBER: US/09/895,828
CURRENT ETLING DATE: 2001-06-28
SUMBER OF SDD ID MOS: 473
SUMBER OF SDD ID MOS: 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 371
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3706
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121 AATGCCCCATATTAAAAGAACTCATTCATAGGAAGGTGTTTCATTTTGGTGTGCAACCCT 180
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                                                                                   361
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                                                                                                                                                                                                                                                              TTAAAAGATGCCTTAATCCATTCCTTGAGGACAGACCTTAGTTGAAATGATAGCAGAATG 3765
                                                                                                                                                                                                                                                                                                                         GTCATTACGTCAACGCAACGTCTAACTGGACTTCCCAAGATAAATGGTACCAGCGTCCTC 240
                                                                                                                                                                                                                                                                                                                                                                GTCATTACGTCAACGCAACGTCTAACTGGACTTCCCCAAGATAAATGGTACCAGCGTCCTC 3705
                                                                                                                     ATTCTCTTCAGTGAATTTTGATAATGGCTTCCAGACTCTTT-GCGTTGGAGACGCCTGTT 3883
                                                                                                                                                                                                                                           TTAAAAGATGCCTTAATCCATTCCTTGAGGACAGACCTTAGTTGAAATGATAGCAGAATG 300
                                                                                 ATTCTCTTCANTGAATTTTGATAATGGCTTCCAGACTCTTTGGCGTTGGAGACGCCTGTT
                                                                                                                                                            TGCTTCTCTCTGGCAGCTGGCCTTCTGCTTCTGAGTTGCACATTAATCAGATTAGCCTGT
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Pred. No. 1e-90;
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: NAME/KEY: mlsc_feature

: LOCATION: (1)...(445)

: OTHER INFORMATION: n = US-09-867-701-9869
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                                                                                                                                                                                                                                             : LENGTH: 422

: TYPE: DNA

: ORGANISM: Bos teurus

: ORGANISM: Bos teurus

: OFFICE INFORMATION: CLONE ID: 30-LIB3058-041-01-K1-H9

US-09-960-52-6956
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US-09-960-352-6996
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APPLICANT: Tao, Manghing
APPLICANT: Byatt, John C.
APPLICANT: Wathlalagan, Magappan
APPLICANT: Mathlalagan, Magappan
TITLE OF INVENTION: UNICLE ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MISCLE AND FAT DEPOSITION
FILE REPERBENCE 16511.006/37-21/10208/C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 6996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6996, Application US/09960352 Patent No. US20020137139A1 GENERAL INFORMATION:
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                                        2313
                                                                                                                        2253 CACCAATGGGCGGCTTCCAGTCAAGTGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATA 2312
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  95
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                                                                                                                                                             Match 7.5%;
Local Similarity 90.5%;
Les 352; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCCATCAGAGCGATGTCTGGTCCTTCGGGGTGTTAATGT-GGAGATCTTCACGTTAGG 153
                                     CACTCATCAGAGTGATGTCTGGTCCTTCGGGGTGTTAATGTGGGAGATCTTCACTTTAGG 2372
                                                                                CTCGCAGGGCCGACTTCCGGTCAAGTGGATGGCTCCCGAAGCCCTTTTCGACAGAGTGTA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTATAACGTTAATTATTAATAAATTGGTAATATACAAA 1
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ilarity 99.0%;
Conservative
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Pred. No. 5.7e-82;
                                                                                                                                                                              Score 319.4; DB 10; Length 422; Pred. No. 1.2e-64;
                                                                                                                                                                Mismatches
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APPLICANT: Wany, Tongtong on APPLICANT: WANGILL, Patricia D. APPLICANT: Watanabe, Yoshihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 446
LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Garter, Darrick
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCEN
FILE REFERENCE: 101012.539
CURRENT APPLICATION NUMBER: US/09/895,828
CURRENT APPLICATION OFFE: 2001-06-28
NUMBER OF SEO ID NOS: 4701-06-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. US20020099012A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                    3471 TATCAGATCCTTTGAAAAGAGAATATTTACAATATATGACTAATTTGGGGAAAATGAAGT 3530
                                                                                                                                                                                                                                                                                                            3531 TTTGATTTATTTGTGTTTAAATGCTGCTGTCAGACGATTGTTCTTAGACCCTCCTAAATGC 3590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 6.9%; Score 294; DB 10; Local Similarity 100.0%; Pred. No. 7.6e-59;
                                                                                                                                                                                                                                                                                                                                                                          1 TATCAGATCCTTTGAAAAGAGAATATTTACAATATATGACTAATTTGGGGAAAATGAAGT 60
                                                                                                                                                                                 CCOATATTAAAAGAACTCATTCATAGGAAGGTGTTTCATTTTGGTGTGCAACCCTGTCAT 3650
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                                                                                                                                       TACGTCAACGCAACGTCTAACTGGACTTCCCCAAGATAAATGGTACCAGCGTCCTCTTAAA 3710
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                                             AGATGCCTTAATCCATTCCTTGAGGACAGACCTTAGTTGAAATGATAGCAGAAT 3764
                                                                                          TACGTCAACGCAACGTCTAACTGGACTTCCCAAGATAAATGGTACCAGCGTCCTCTTAAA
                                                                                                                                                                                                                                                                               TTTGATTTATTTGTGTTTAAATGCTGCTGTCAGACGATTGTTCTTAGACCTCCTAAATGC 120
AGATGCCTTAATCCATTCCTTGAGGACAGACCTTAGTTGAAATGATAGCAGAAT 294
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; ORGANISM: Drosophila melanogaster
US-10-108-605-250
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PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID MOS: 361
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 250
LENGTH: 2782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DEOSOPHILA RELANGASTER THAT ENCODE TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF FILE REFERENCE: 31133B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/761,142 PRIOR FILING DATE: 2001-01-16
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GTTTGATAGAGTATACACTCATCAGAGTGATGTCTGGTCCTTCGGGGGTGTTAATGTGGGA 2357
                                                         CTATTACAAAAAGACCACCAATGGGCGGCTTCCAGTCAAGTGGATGGCTCCAGAAGCCCT 2297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTCTATGTCATAGTTGAGTATGCCTCTAAAGGCAACCTCCGAGAATACCT------
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                                     CGATGATTATGTGCTGAAGATTGCTGATTTTGGACTGGCGAGGGATATCCAAAGCACGGA 1818
                                                                                                                                                              AGAAAACAATGTGATGAAAATAGCAGACTTTGGACTCGCCAGAGATATCAACAATATAGA 2237
                                                                                                                                                                                                       CTATTTGGCCTCGCGGCGATGCATCCATCGAGATTTGGCAGCCAGGAATCTGCTCGTCAG
                                                                                                                                                                                                                                               GTACTTGGCTTCCCAAAAATGTATTCATCGAGATTTAGCAGCCAGAAATGTTTTGGTAAC
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59.3%;
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Pred. No. 5.4e-54;
0; Mismatches 333;
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; OTHER INFORMATION: n = A,T,C
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APPLICANT: WEI, MING-Hui et al
APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING I
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001174
CUBRENT APILCATION NUMBER: US/09/814,950
CUBRENT FILING DATE: 201-03-23
NUMBER OF SEG ID NOS: 401-03-23
NUMBER: FASTSED for Windows Version 4.0
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Matches
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LENGTH: 33239
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LOCATION: (1)...(33239
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Local Similarity 98.9%; Pred. No. 1.6
hes 273; Conservative 0; Mismatches
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GTGAAACTTGGTACTTCATGGTGAATGTCACAGGTG 30125
                                    GTGAAACTTGGTACTTCATGGTGAATGTCACAGATG 652
                                                                           AGGGCGCCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAGACA 30089
                                                                                                  AGGGCGCCACGCCTAGAGACTCCGGCCTCTATGCTTGTACTGCCAGTAGGACTGTAGACA 616
                                                                                                                                                          ATGGGGTGCACTTGGGGCCCAACAATAGGACAGTGCTTATTGGGGAGTACTTGCAGATAA 30029
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1.6e-52;
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US-09-731-872-128 : Sequence 128, Application US/09731872 ; Patent No. US20020102604A1

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NAME/KEY: CDS
LOCATION: 179..427
NAME/KEY: sig_peptide
LOCATION: 179..298
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LOCATION: Secre 7.72883276007822
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APPLICANT: DOUBLE Edwards, Jean Baptiste
APPLICANT: Bouqueleret, Lydie
APPLICANT: Bouqueleret, Lydie
APPLICANT: Bouqueleret, Lydie
APPLICANT: BOUQUELERET, BEWERTHUARN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
TITLE OF INVENTION: CULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
TILLE REPERRNCE: 78.U33.REG
CURRENT APPLICATION AVMERE: US/09/731,872
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION AVMERE: US 60/189.629
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 399-12-08
PRIOR FILING DATE: 399-12-08
PRIOR FILING DATE: 2000-03-06
NUMBER 0F SEG ID NOS: 482
SOPTMARE: Patent.pm
SEQ ID NO 148
SEQ ID NO 148
TYPE: 1486
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Best Local Similarity 99.6
Matches 263; Conservative
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ORGANISM: Homo sapiens
FEATURE:
322 GGATACCACATTAGAGCCAGAAGA 345
                        360 GGATACCACATTAGAGCCAGAAGA 383
                                                                                 240 ATATGGAAGAGGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTG 299
                                                                                                                                                                                                                                                               180 ATTOCCCCTACTCCATCCCCCTACAGGAACTTCCACATCGGATTAACCTTCACATTGGAC 239
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92 CCAGTGACTGCAGCAGCAGCAGCGCGCAGCGCTGGGTTCCTGAAGCC 141
                                                                                                                                                                           202 ATATCGAACACGACCGGGGATTGGTACCGTAACCATGGTCAGCTGGGGTCGTTTCATCTG
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Search completed: December 11, 2002, 17:40:36 Job time :  $388\ \text{secs}$ 

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18829.294 Million cell updates/sec
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## ALIGNMENTS

FEATURES SOURCE	JOURNAL COMMENT	TITLE	REFERENCE	SOURCE	ACCESSION VERSION	RESULT 1 BQ438964 LOCUS DEFINITION
Email: ogaphs remail.nih.gov Tissue Procurement: ATC: Tissue Procurement: ATC: CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Cione distribution: MCC clone distribution Information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAN1218 row h column: 01 High quality sequence stop: 770. 1885	Unpublished (1999) Contact: Robert Strausberg, Ph.D.	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	EURATYODA; MEDAZOA; CHORGAGA; CEANAGA; VERTEDERIA; EULELHOSCIONA; Mammalia; EUtheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 885)	human. Homo sapiens	E0,38964 B0,38964 B0,38964.1 GI:21178040	BQ438964 885 bp mRNA linear EST 24-MAY-2002 AGENCOURT_7761624 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6018096

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Query Match
Best Local Similarity
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                     GTTTCTGGAGCAGTGGACTGCCACAAGCCACCATGTAACCCCTCTCACCTGCCGTGCGTT
                                                                 CTTGTTGTCTCCACTTGTATATATGGATCAGAGGAGTAAATAATTGGAAAAGTAATCAGC
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TTTTCTGGAGCAGTGGACTGCCACAAGCCACCATGTAACCCCTCTCAACTGCCGTGCGTA
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TITLE
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2593 CAACCTCTCGAACAGTATTCACCTAGTTACCCTGACACAAGAAGTTCTTGTTCTTCAGGA
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g0449j09:x1 Soares_pregnant_uterus_NBHPV Homo saplens cohA cione
1MADE:1712704 3' Similar to gb:MR97770 EIRBOBLAST GROWTH FACTOR
RECEPTOR 2 PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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/clone="IMAGE:1712704"
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/lab_host="DH108"
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AU132307
AU132307.1
                                                         Email: genomicsehri.co.jp

HRI human cDNA project; 5', 6 3' end one pass sequencing: Helix

Research Institute: cDNA library construction: Department of

Vicology, Institute of Hedical Science, University of Tokyo, and

Helix Research Institute.
                                                                                                                                             Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
                                                                                                                                                                                     Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                           Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Isogai,T.
                                                                                                                                                                                                                                                                 Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K.,
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1 (bases 1 to 803)
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AU132307 NT2RP3
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/organism="Homo sapiens"
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                                                                                                                    CTACCAGCTGGCCAGAGGCATGGAGTACTTGGCTTCCCAAAAATGTATTCATCGAGATTT 215:
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/cell_type-"teratocarcinoma"
/cell_line="Mr2"
/cell_line="Mr2"
/note="wector: pwEl8SF13; mRNA from NT2 neuronal cells after 2-weeks retinoic acid (RA) induction*
a 193 c 210 g 166 t 3 others
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BQ879891 LOCUS

DEFINITION

BQ879891 987 bp mRNA linear EST 16 AGENCOURT\_8232182 Lupski\_dorsal\_root\_ganglion Homo sapiens

EST 16-AUG-2002

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AUTHORS
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hes 791; Conserv
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                                                                                                                                                                                                                                                  TTGTTCTTCAGGAGATGATTCTGTTTTTTCTCCCAGACCCCATGCCTTACGAACCATGCCT 2699
                    ATATGTGTAAAGATTTATACAGTTGAAAACTTGTAATCTTCCCCAGGAGGAGGAAGAAGGT 2939
                                                                             CTTGTTGTCTCCACTTGTATATATGGATCAGAGGAGTAAATAATTGGAAAAGTAATCAGC
                                                                                               CTTGTTGTCTCCACTTGTATATATGGATCAGAGGAGTAAATAATTGGAAAAGTAATCAGC
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BQ879891
BQ879891.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ogapbs-rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski
DDNA Library Properation: Life Tocholgies, Inc.
DNA Library Arrayed by: The I. M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Biostiance Corporation
Chome distribution: MGC_clone distribution information can
found through the I.M.A.G.E. Consortium/Linl.at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 987)
NHH-MCC http://mgc.ncl.nlh.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLAM13569 row: c column:
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Mammalia; Eutheria;
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1 kb for average insert length 17 kb, This is a primary
1 thrary, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylo
coliege of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="vector: pCMV-SPORT6 (Life Technologies); Site_1: Not1; Site_2: Sh1; cDMA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="dorsal root
/dev_stage="adult, 36 yr"
/lab_host="DH108"
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/clone_1ib="Lupski_dorsal_root_ganglion"
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1. .987
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae;
1 (bases i to 834)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammailan Gene Colle
                                                                                                                                                                                                Sequencing by: Incyte Genomics, Inc. Clone distribution information Clone distribution information found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                       Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life TechnolocDNA Library Arrayed by: The I.M.A.G.E.
                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
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   A1081876 1747 bp mRNA linear EST-24-ESP-1998 ox778-01.x1 Soares_NhHMPu_S1 Home sapiens cDNA clone HAGE:1662312 37 similar to 90:M87770 FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (HUMAN); mRNA sequence.
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                                                                                                GCTTCTGAGTTGCACATTAATCAGATTAGCCTG-ATTCTCTTCAGTGAATTTTTGATAATG
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Seg_primer: -0ml3 fwd. ET from Amersham
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Email: cgapbs-r@mail.nih.gov
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National Cancer Institute, Cancer Genome Ana
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Mammalia; Eutheria;
l (bases 1 to 747)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: mixed (see below); Vector: p773D-Pac (Pharmacia) with a modified polyllnker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plesmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus were made an vitro: Following MAP purification. this DNA was used as tracer in a subtractive, hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pregnant uterus"
/lab_host="DH10B"
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/clone_lib="Soares_NhHMPu_S1"
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Pred. No. 1.9e-135;
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through IMAGE Consortium (info@image.llnl.gov) for figners Length: 895 Std Error: 0.00
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755 bp mRNA linear EST 13-APR-1959
th78g05: X1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2124824
3, similar to dp:H87770 FIBROBLASE
3, precursor (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
Contact: Robert Strausberg, Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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1 (bases 1 to 755)
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Location/Qualiflers
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                                                                were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5.000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. Clones 260232-265223, 3040488-345479, and 46488-84479.
                                                                                                                                                                                      note Organ: mixed (see below); Vector: p773D-Pac (Pharmacia) with a modified polylinker; site_1: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte ZNBHM, pregnant uterus NBHPU, and fetal heart NBHBIN) were mixed, and ss circles
                                                                                                                                                                                                                                                                           /lab_host="DH108"
                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone='IMAGE:2124824"
/clone_Ilb-"Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart,
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  16.1%;
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Primates;
  Score 686.8; DB 9;
Pred. No. 3.7e-135;
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                                               Eukaryota; Metazoa; Che
Mammalla; Eutherla; Pr
1 (bases 1 to 693)
Kim, N.S., Hahn, Y., Oh.;
Oh, K.J., Cheong, J.E., 9
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Unpublished (2002)
                Kim, Y.S.
21C Frontier Korean
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K-EST0072606 S22SNU16n1 Homo
5', mRNA sequence.
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                                                                  Oh, J.H.,
                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                 GCACACAGGATGGGCCTCTCTATGTCATAGTTGAGTATGCCTCTAAAGGCAACCTCCGAG
                                                                                                        AGATGGAGATGATGAAGATTGGGAAACACAAGAATATCATAAATCTTCTTGGAGCCT
                                                                                                                                  AGATGGAGATGATGAAGATGGGAAACACAGAATATCATAAATCTTCTTGGAGCCT 193:
                                                                                                                                                                                                    TGGCCGTGAAGATGTTGAAAGATGATGCCACAGAGAAAGACCTTTCTGATCTGGTGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: yongsung@mail.kribb.re.kr
Plate: 28 row: B column: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kim YS
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/lab_host="DH10B"
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/cell_line="SNU-16"
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Pred. No. 8.6e-134;
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NEtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo,
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/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Pooled human melanocyte, fetal heart,
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                                                                                                                                                                                   Score 675.6; DB 9;
Pred. No. 8.7e-133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGATTACACTGATCTTATGTGTTACAAAATTGGAGAAAGTATTTAATAAAACCTGTTAA 4180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGGGGATACGTCCATCTTTTAAGGGATTGCTTTCATCTAATTCTGGCAGGACCTCACC 4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGGGATACGTCCATCTTTTAAGGGATTGCTTTCATCTAATTCTGGCAGGACCTCACC
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UI-CF-EC1-abu-b-07-0-UI.sl UI-CF-EC1-lehos sapiens cDNA clone
UI-CF-EC1-abu-b-07-0-UI 3', mRNA sequence.
                University of Iowa
2024 University of Iowa
Tel: 319 356 4866
Fax: 319 356 7171
                                                                                                                  Contact: McCray, PB
                                                                                                                                                        Genome Res. 6 (9),
                                                                                                                                                                                                                                                                                                                                                      BM970064.1 GI:19587651
Ema j. 1 :
                                                                                               McCray Lab
                                                                                                                                                                           discovery
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Bonaldo, M.F., Lenno
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paul-mccrayeulowa.edu
                                                                                                                                                                                                                 Lennon, G. and Soares, M.B
                                                                                                                                                        791-806 (1996)
                                                         Med Labs, Iowa City,
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                                ATAATTGGAGAAGATTTATGTCAGCACACACTTACAGAGCACAAATGCAGTATATAGGTG 3119
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                                                                                                                                                                                                                                                                                                                CTTGTTGTCTCCACTTGTATATATGGATCAGAGGAGTAAATAATTGGAAAAGTAATCAGC
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Conservative

15.8%; 0

Score 675; DB 14; Pred. No. 1.2e-132; Mismatches

Length 690; Indels

0, Gaps

0

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451

571

271

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Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 1-66, >AT_richia_complexity (matched compliment) 216-266, >CMA in Fishiple_repeat seq.primer: Mil FORMARD
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DNA Library preparation: Dr. M. Bento Soares, University of lows 
DNA Library Arrayed by: Dr. M. Bento Soares, University of lows 
DNA Sequencing by: Dr. M. Bento Soares, University of lows 
DNA Sequencing by: Dr. M. Bento Soares, University of lows 
Clone Distribution: Researchers may obtain clones from Research
         210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /iab host blook title Technologies) (T) phage resistant, //note forgan: Lung, Vector: pT713-Pac (Pharmacla) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; U1-CF-ECI is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dry primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digsted with Not I, and cloned directionally into pT773-Pac vector. The oligonachectide used to prime the prime contains and prime containing a strander containing a magnetic purpose of the prime that prime containing a prime prime containing a prime p
TAG_SEQ=AAGTGCTTAC"
a 136 c 120 g
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TAG_LIB=UI-CF-EC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xre"ut=xcon:9606"
/clone="UT-CF-EC1-abu-b-07-0-UI"
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                                                                                                                                                                                                             TAG_TISSUE Normal Lung
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                           3159 ATATTATATATTACAAGGAGTTATTTTTTGTATTGATTTTAAATGGATGTCCCAATGCA 3218
                                                                           3099 CACAAATGCAGTATATAGGTGCTGGATGTATGTAAATATTTCAAATTATGTATAAATAT 3158
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AV726725
AV726725
                                                                                                                                                                                                                                                                                                                                                                                       Email: hanzg@chgc.sh.cn
This clone is available at CHGC
                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                    Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Zeguang H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens cDNA HTC clones
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Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu
,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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	CAGAATGTGCTTCTCTGGCAGCTGGCCTTCTGCTTCTGAGTTGCA 3805	3759	Qy
660	CGTCCTCTTAAAAGATGCCTTTATCCATTTCCTGAGGACAGACCTTAATTGAAATGATAG	601	οb
3758	CGTCCTCTTAAAAGATGCCTTAATCCATTCCTTGAGGACAGACCCTTAGTTGAAATGATAG	3699	40
600	CAACCCTGTCATTACGTCAACGCAACGTCTAACTGGACTTNCCAAGATAAATGTTACCAG	541	DЪ
3698		3639	Qy
540	CCTCCTAAATGCCCCCATATTAAAAGAACTCATTCATAGGAAGGTGTTTCATTTTGGTGTG	481	В
3638		3579	Qy
480	GGAAAATGAAGTTTTGATTTATTTGTGTTTAAATGCTGCTGTCAGACGATTGTTCTTAGA	421	В
3578	-	3519	Ϋ́
420	GACTTAACTAGTTATCAGATCCTTTGAAAAGAGAATATTTACAATATATGACTAATTTGG	361	망
3518	GACTTAACTAGTTATCAGATCCTTTGAAAAAGAGAATATTTACAATATATGACTAATTTGG	3459	Qy
360	TTGTAATTTAAGTGGCATTTCTATGCAGGCAGCAGCAGACTAGTTAATCTATTGCTTG	301	В
3458		3399	Qγ
300	TAACGTTAATTTATTAATAAATTGGTAATATACAAAACAATTAATCATTTATAGTTTTTT 3	241	ď
3398	TAACGTTAATTAATAAATAGGTAATATACAAAACAATTAATCATTATAGTTTTTT	3339	Qy
240	ATTTCTTAATTTTCACCGAGCAGAGGTGGAAAAATACTTTTGCTTTCAGGGAAAATGGTA 2	181	ď
3338	ATTTCTTAATTTTCACCGAGCAGAGGTGGAAAAATACTTTTCCTTTCAGGGAAAATGGTA	3279	Qγ
180	CCTAGAAAATTGGTCTCTCTTTTTTTAATAGCTATTTGCTAAATGCTGTTCTTACACATA	121	₽
3278		3219	Ş

ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION COMMENT REFERENCE AUTHORS TITLE JOURNAL 693 bg mRNA linear EST 19-JUN-UI-H-EZI-bbh-g-l1-0-UI.sl NCI\_CGAP\_CL2 Homo saplens cDNA clone UI-H-EZI-bbh-g-l1-0-UI 3', mRNA sequence. BQ575816 BQ575816.1 GI:21479133 Contact: Robert Straubberg, Ph.D. Email: Cgapbs-rémail.nih.gov Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia: Eutheria; Primates; Catarrhini; Hominidae: 1 (bases 1 to 693) Unpublished (1997) Tumor Gene Index Homo sapiens Hominidae; Homo Euteleostomi; EST 19-JUN-2002

DNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Cione Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@iowa.edu
The following repetitive elements were found in this cDNA sequence: 1-46, >AT\_richiow\_complexity (matched compliment)
217-267, >TA);neSimple\_repeat

Orthoapedics

of.

Seq primer: POLYA-Yes.

M13 FORWARD

RESULT 12 BQ575816/c

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                          TTTTTTTAATAGCTATTTGCTAAATGCTGTTCTTACACATAATTTCTTAAATTTTCACCGA 3297
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TAG_LIB-UI-H-E21
TAG_TISSUE_grade-2-chondrosarcoma
TAG_SE0-ATCTAATATG*
135 c 123 g 223 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_Ch2"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
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/clone="UI-H-EZ1-bbh-g-11-0-UI"
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Pred. No. 9.7e-131;
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CTGGAGATAGCCATTTACTGCATAGGGGTCTTCTTAATCGCCTGTATGGTGGTAACAGTC 1458
                                                                                                                                               CTGGAGATAGCTATTTACTGCATAGGGGTCTTCTTAATCGCCTGCATGGTGGTGACAGTC 120
                                                                       ATCCTGTGCCGAATGAAGAACACGACCAAGAAGCCAGACTTCA-GCAGCCAGCCGGCTGT 1517
                                                                                                                                                                                                                                                                                                    GGTTGACAGTTCTGCCAGCGCCTGATGAGAGAGAGAGGAGATCACGGCTTCCCCAGATTAT 60
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Tissue
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Plate: LLAM11893 row: m column:
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Clone distribution: MCC clone distribution information can
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Site_2: NotI (Cloned unidirectionally, Primer: 01jo dT.
Library constructed by Life Technologies. Investigators
providing samples; Lothar Hendighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
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/clone="IMAGE:5351597"
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0; Mismatches 79;
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MAGE:5351597 5',
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1518 GCACAAGCTGACCAAACGTATCCCCCTGCGGAGACAGGTAACAGTTTCGGCTGAGTCCAG 1577

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REFERENCE
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                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.n1h.gov
Tissue Procurement: Lothar Hennighausen
                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                         Mammalla; Eutheria; Rodentia; Sciurognat)
1 (bases 1 to 787)
1 (hases 1 to 787)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian
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Eukaryota; Metazoa;
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CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M. A.G.E. Consortium (LIN DNA Sequencing by: Incyte Genomics, Inc. Conformation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LiMu at:
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Sciurognathi; Muridae; Murinae; Mus
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                                                   GCTTCCAGTCAAGTGGATGGCTCCAGAAGCCCTGTTTGATAGAGTATACACTCATCAGAG
                                                                                                                          CTTTGGACTCGCCAGAGATATCAACAATATAGACTATTACAAAAAGACCACCAATGGGCG
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                                  ACTTCCAGTCAAGTGGATGGCTCCTGAAGCCCTTTTTGATAGAGTTTACACTCATCAGAG
                                                                                                         CTTTGGCCTGGCCAGGGATATCAACAACATAGACTACTATAAAAAGACCACAAATGGGCG
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Site_2: NotI: Cloned unidirectionally, Primer: Oliso dT.
tabrary constructed by Life Technologies. Investigators
providing samples: Lothar Hennighousen/Priscilla Furth,
NIH Reference for transpenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:5351304"
/clone_lib="NCI_CGAP_Mam4"
/tlssue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
I (Dages 1 to 852)
NIH-MCC http://mgc.ncl.hl.gov/.
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Tissue Procurement: Lothar Hennighausen Ph.D.,
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/tlssue_type="tumor, gross tissue"
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Search completed: December 11, Job time : 3758 secs 2002, 17:35:12

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us-10-090-035-25	US-10-047-593-6	US-09-950-933A-99	US-10-034-451-1	US-09-864-785-3499	US-09-864-785-3425	US-09-864-785-3338	US-09-864-785-3109	US-09-827-289-25	US-09-827-289-21	US-09-827-289-16	US-09-827-289-12	US-09-245-802-45	-07	073-881	US-09-073-881-4	US-09-732-914-80	US-09-732-914-73	US-09-732-914-68	US-09-864-785-3578	US-09-996-634-144	80-887-1	US-09-465-802-32		-09-864-785-	US-09-864-785-3333	
N		99		34		Sequence 3338, Ap	3109,	25,	21	16,	12,	45	26,	24	Sequence 4, Appli	90,	73,	Sequence 68, Appl		144	9	e 32	3501,		Sequence 3333, Ap	

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### ALIGNMENTS

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Sequence 25, Application US, Patent No. US20020009716A1; GENERAL INFORMATION; APPLICANT: APPLICANT:
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US-09-801-274-958
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Patent No. US20020032319A1
GENERAL INFORMATION:
                                                 GENERAL INFORMATION:
APPLICANT: Abarzua, Patricio
TITLE OF INVENTION: Process for Allele Discrimination Using Primer
TITLE OF INVENTION: Extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 958
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Best Local Similarity 83.9%;
Matches 26; Conservative
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APPLICANT: Lander, Erle
APPLICANT: Lander, Erle
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 3823.2009-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
FILE REFERENCE: 469290-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/206,129 PRIOR FILING DATE: 2000-05-22
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Pred. No. 7
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RESULT 4
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US-09-801-274-957
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local Similarity 80.6%;
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Best Local Similarity
  SEQ ID NO 1012
                 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIGENOSIS OF COLON CANCER PLLE REFERENCE: 201121.504
CURRENT PRILICATION NUMBER: US/09/815,343
CURRENT FILMS DATE: 2011-03-22
SOPTMARE: 380 TO NOS: 1556
SOPTMARE: 38158D for MAINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE FOLYMORPHISMS
FILE REFERENCE: 2835.2009-001
CURRENT APPLICATION UNMERE: US/99/801,274
CURRENT FILING DATE: 2001-03-07
                                                                                                                                         APPLICANT: Meagher, Madeleine
APPLICANT: Xu, Jiangchun
APPLICANT: King, Gordon E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
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CURRENT FILING DATE: 2001-04-05
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: use in allele discrimination
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Pred. No. 1.8e+04;
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Pred. No. 1.5e+04;
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                                                                                                                                                             SEQ ID NO 22
LENGTH: 46
Query Match
Best Local Similarity
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Best Local Similarity
Matches 31; Conserv
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TYPE: DNA
                                                                                                                                              TYPE: DNA
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US-09-827-289-22/c : Sequence 22, Application US/09827289
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US-09-815-343-1012
                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Abarzua, Patricio
TITLE OF INVENTION: Process for Allele Discrimination Using Primer
TITLE OF INVENTION: Excension
FILE REPERANCE: 469290-5
CURRENT APPLICATION UNBER: US-05/827,289
CURRENT APPLICATION NUMBER: US-05/94843
PRIOR PPILICATION NUMBER: US-05/194843
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                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. US20020009716A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 469290-55
CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT FILLING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: U.S. 60/194843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Process for Allele Discrimination Using Primer TITLE OF INVENTION: Extension
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                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
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Description of Artificial Sequence: use in allele discrimination
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Pred. No. 2.5e+04;
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Pred. No. 2.3e+04;
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Score 22; Pred. No.

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US-09-864-785-3604; Sequence 3604, Application US/09864785
                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: use in allele discrimination
US-09-827-289-24
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Best Local Similarity
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
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SEQ ID NO 13
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Patent No. US20020068059A1
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                                                                                                                                                                                                                                                                                                                                                                                             TYPLE OF INVENTION: Process for Allele Discrimination Using Primer TIPLE REFERENCE: 460290-55 CURRENT APPLICATION NUMBER: US/09/827,289 CURRENT PLING DATE: 2001-04-05 PRIOR APPLICATION NUMBER: US. 60/194843 PRIOR APPLICATION NUMBER: US. 60/194843 PRIOR FILING DATE: 2000-04-05 PRIOR FILING DATE: 2000-04-05 PRIOR PILING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: U.S. 60/194843
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CURRENT APPLICATION NUMBER: US/09/875,519A
CURRENT FILING DATE: 2001-66-0687/00603
PRIOR APPLICATION NUMBER: PCT/GB97/00603
PRIOR FILING DATE: 1997-03-04
NUMBER OF SED ID NOS: 35
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                TYPE: DNA
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Pred. No. 3
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Pred. No. 3.4e+04;
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  CURRENT APPLICATION NUMBER: US/09/827,289
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RESULT 11
US-09-827-289-20
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; OTHER IMPORMATION: use in allele discrimination
US-09-827-289-26
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US-09-864-785-3604
Sequence 20, Application US/09827289
Patent NO. US2002009916A1
RENERAL INFORMATION:
APPLICANT: Abarzas, Patricio
TITLE OF INVENTION: Process for Allele Discrimination Using Primer
TITLE OF INVENTION: Excension
FILE REPERSENCE: 46920-5
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Best Local
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SEQ ID NO 26
LENGTH: 46
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Best Local Similarity
Matches 20; Conserv
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CURRENT APPLICATION NUMBER: US/09/827,289
CURRENT FILMC DATE: 2001-04-05
PRIOR APPLICATION NUMBER: U.S. 60/194843
PRIOR FILMS DATE: 2000-04-05
NUMBER OF SEO ID NOS: 35
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TITLE OF INVENTION: Process for
TITLE OF INVENTION: Extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Enzymatic Nucleic Acid
TITLE OF INVENTION: Levels of NF-Kappa B
FILE REFERENCE: 400/022 (MBHB00-812-D)
CURRENT APPLICATION NUMBER: US/09/864,785
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 3929
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Draper, Ken
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Pred. No. 3.8e+04;
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Pred. No. 3
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; OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: use in allele discrimination US-09-827-289-24
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PRIOR APPLICATION UNMER: U.S. 60/
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Vgr. 2.1
SEQ ID NO 20
LENGTH: 46
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Best Local S
Matches 28
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                                                                                                        APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US. 60/194843
PRIOR FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Process for Allele Discrimination Using Primer TITLE OF INVENTION: Extension FILE REFERENCE: 469290-55
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  APPLICANT: PAIK, SO-JUNG
TITLE OF INVENTION: MADDARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THEREFOR
TITLE OF INVENTION: AND USES THEREFOR
                                                                       APPLICANT:
                                                                                         APPLICANT:
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FILE REFERENCE: 00-653-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                        Storhoff, James J.
Elghanian, Robert
                                                                                                                                                              Mucic, Robert C.
                                                                       Li, 2hi
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                                                                                                           Thomas A.
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; Pred. No. 4.3e
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Pred. No. 4.3e+04;
0; Mismatches 11;
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PRIOR APPLICATION NUMBER: 09-240.755
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: CCT/US97/12783
PRIOR APPLICATION NUMBER: CCT/US97/12783
PRIOR PRILING DATE: 1997-07-21
PRIOR PRILING DATE: 1998-07-29
PRIOR FILING DATE: 2000-01-38
PRIOR PRILING DATE: 2000-01-38
PRIOR PRILING DATE: 2000-01-38
PRIOR PRILING DATE: 2000-01-38
PRIOR FILING DATE: 2000-01-38
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PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: 60/224,631
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/224,392
PRIOR FILING DATE: 2000-12-08
PRIOR PPLICATION NUMBER: 60/255,235
PRIOR FILING DATE: 2000-12-11
PRIOR PPLICATION NUMBER: 60/255,235
PRIOR FILING DATE: 2000-12-11
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Best Local Similarity
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SEQ ID NO 72
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PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/603,830
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PRIOR APPLICATION NUMBER: 09/344,667
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PRIOR FILING DATE: 2001-03-28
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APPLICANT:
APPLICANT:
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                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3166 ATATTTACAAGGAGTTATTTTTTTGTATTTGATTTT 3199
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                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               COUNTRY: U
ZIP: 20004
                                                                                                                                                       CITY: Washington D.C.
                                                                                                                                                                             STREET:
                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 ATATTGATAAGGATTTTTTTTTTTTTTTTTTTTTTT
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                                                                                                                                                                             E: Jacobson, Pr.
400 Seventh St.
                                                                                                                                                                                                                                                                                      Kurecki, Tomasz
Gollhick, Paul D.
Doyle, Darrell J.
TVENTION: Cloning, Expression,
                                                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                                                                                                                             Kruzel, Marian L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%;
76.5%;
                                                                                                                                                                                                                                                                       Lactoferrin
                                                                                                                                                                             Price, Holman & Stern
St. N.W.
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Pred. No. 4.1e+04;
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Version #1.25
                                                                                                                                                                                                                                                                                         and Uses of Human
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-828-592-2
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US-09-828-592-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
Search completed: December 11, 2002, 20:51:22 Job time: 122 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPOMUNICATION INFORMATION:
TELEPINE: (202) 53-666
TELEPIN: (202) 393-3550
IMPORMATION FOR SAD IN: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TEPE: INCLUDED SCILITS
TEPE: INCLUDED SCILITS
TEPE: INCLUDED SCILITS
                                                                                                                                                                 Ouery Match 0.5%; Score 20.8; DB 10. Best Local Similarity 70.0%; Pred: No. 5. 6e+04; Matches 28; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/828,592
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION UNMBER: 60/195,872
PRIOR FILING DATE: 2000-04-07
NUMBER OF 5EQ ID NOS: 15
SOFTMARE: Batentin Ver. 2.1
SED ID NO 2
SED ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09828592 Patent No. US20010055591A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.5
Best Local Similarity 70.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Walston, Timothy
APPLICANT: Cooper, Sout
APPLICANT: Reviale, Altreae
TITLE OF INVENTABLE, ANTITHROMBIN H-HELIX MUTANTS
FILE REFERRNCE: 7869.100501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: U5/08/724,586
FILING DATE: 30-SEPT-1296
APPLICATION NUMBER: U5 08/238,445
FILING DATE: 05 08/238,445
APTGRAY ON NUMBER: U5 08/238,445
APTGRAY ON NUMBER: 13,409
REFERENCE/DOCKET NUMBER: 13,505/P581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: SI
TOPOLOGY: linear
MOLECULE TYPE: DN/
MYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1467 CCGAATGAAGAACACGACCAAGAAGCCAGACTTCAGCAGC 1506
                                                                                                     843 GTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGC 882
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APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 CCCGAGGAAGAACAGGACGAGGAAGACAAGTTTCATAAGC 3
                                                                             3 GTGGCTGAAAAAATTGAAGAAGATGATGCTGGTGGTTCAC 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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# GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

December 11, 2002, 17:35:24; Search time 367; Seconds (Without alignments) Seconds 18829:294 Million cell updates/sec

Title: Perfect score: Sequence: 

Scoring table: IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: Searched: 16154066 seqs, 8097743376 residues

102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

em\_estin:\*
em\_estmu:\*
em\_estov:\*
em\_estpl:\* em\_estro:\* em\_htc:\* em\_esthum: \* em\_estba:\*

gb\_est1:\*
gb\_est2:\*
gb\_htc:\*
gb\_est3:\*
gb\_est4:\*
gb\_est5:\*
em\_estfin:\* em\_gss\_hum:\* em\_gss\_inv:\* gb\_gss:\* em\_estom: \*

em\_gss\_other:\*
em\_gss\_pro:\*
em\_gss\_rod:\* em\_gss\_pln:\*
em\_gss\_vrt:\*
em\_gss\_fun:\*
em\_gss\_mam:\*
em\_gss\_mus:\*

Pred. No. is the number of results predicted by chance to have a score ogreater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

0	Ų	4	w	c 2	c 1	Result
24.2	24.2	24.2	24.4	25.4	26.2	Score
0.6	0.6	0.6	0.6	0.6	0.6	Query Match Length DB ID
49	49	45	50	43	47	ength 1
9	9	12	9	10	12	. B
AL660945	AL649742	BF582680	AA120437	AV832677	BF107886	esult Query No. Score Match Length DB ID
AL660945 AL660945	AL649742 AL649742	BF582680 602094085	AA120437 mn47a11.r	AV832677 AV832677	BF107886 601823895	Description

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BG256941 BI493940	BI090256 BI858831 AZ346760 AI624136 AL587874	AII104655 AZ624922 T25667 T25667 ALG60275 ALG48743 ALG48743 ALG52653 ALG52668 BG290798	BM183028 AL795414 BI330882 HSM002946 AJ500405	AA11935 AA11936 AU267061 AA590547 AZ587341 AA855120 AL627881 HSM009939	AL545635 AJ50588 AZ57166 AU25866 AL2873666 AL8873666 AL8873666 BE692186 BE692186 BE692186 BE692186 BE692186 BE692186
AA590944 vm25f02.r BG256941 602370419 BI493940 df106e06.	BI090256 602855121 BI858831 603388748 AZ346760 1M0082F12 AI624136 ts26c11.x AI-587874 AI-587874		BM183028 fw29e09. y AL795414 AL795414 BI330882 602981270 Al038470 Homo sapi AJ500405 AJ500405	AN16935 MD2901.r AN16935 MD2901.r AU267061 MU267061 AN590547 VI06404.r AZ587341 IM0394020 AR853120 NHTBCae03 AL627881 AL627881 AL045089 Homo sap1	AJ500588 AJ500588 0 1M0467L0 AU268686 6 60224725 8 60224725 8 60224917 AU107269 AU107270 Homo sapi

### ALIGNMENTS

FEATURES	COMMENT	TITLE JOURNAL	AUTHORS	REFERENCE		ORGANISM	SOURCE	VERSION	ACCESSION	DEFINITION	RESULT 1 BF107886/c
Email: gapbs remail.nih.gov Tissue Proquement: CLONTECH Laboratories, Inc. DNA Library Proparation: CLONTECH Laboratories, Inc. DNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMGG row: n column: 24 High quality sequence start: 8 High quality sequence start: 8 Ligh quality sequence start: 9 Location/Qualifiers	Contact: Robert Strausberg, Ph.D.	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	NIH-MGC http://mgc.nci.nih.gov/.	<pre>Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo. 1 (bases 1 to 47)</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	BF107886.1 GI:10890412	mRNA sequence. BF107886	601823895R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043735 3',	

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BASE COUNT
ORIGIN
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
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Query Match
Best Local S
Matches 29
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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    29;
                                                                                                                                                                                                                                                                                                                               Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayame University, Barley Germpiasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare subsp. vulgare.
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnollophyta; Lillopsida; Poales; Poaceae; Pooldea;
Trittoeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV832677 4.3 bp mRNA linear kgr 22-JUN-20
AV832677 K. Sato unpublished cDNA library: Hordeum vulgare subsp-
vulgare top three leaves adult, heading stage Hordeum vulgare
                                                                                                                                                                                                                                          URL:http://www.rib.okayama-u.ac.jp/barley/
Sato,K., Saisho,D., Takeda,K., Shini,T. and
                                                                                                                                                                                                                                                                                                    Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/
                                                                                                                                                                                                                                                                         submission;
                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                        Barley EST sequencing project in
                                                                                                                                                                                                                                                                                                                                                                                                                        Sato, K.
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                Similarity
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  *Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library."
a 1 c
                                                                                                                                  /db_xref="raxon:112509"
/clone="pail0b06"
/clone="the fix. Sato unpublished cDNA library: Hordeum
/clone=lib="K. Sato unpublished cDNA library: Hordeum
/vulgare subsp. vulgare top three leaves adult, heading
                                                                        /tissue_type="top three leaves"
/dev_stage="adult, heading stage"
1 c 4 g 31 t
                                                                                                                                                                                            /organism="Hordeum vulgare subsp. vulgare'/cultivar="Haruna Nijo"
              72.5%
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  0,
              Score 25.4; DB 10
Pred. No. 9.8e+05;
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Pred. No. 6.5e+05;
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                             DB 10;
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Indels
                             Length 43;
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RESULT 3
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mes 34; Conser
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                                                                                                                                BF582680 45 bp mRNA linear EST 12-DEC-602094085F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4208373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA120437

50 bp mRNA linear EST 19-NOV-mn47all.rl Beddington mouse embryonic region Mus musculus CDNA clone IMAGE:541052 5', mRNA sequence.

AA120437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Lo,M., Martin,J., Mortis,M., Schellenberg,K., Stepte,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 50)
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                                                                                                                                                                                                                                                                                                                                        from CS7BL6 x DBA matings, excluding embryos that had developed head folds and all extraembryonic tissues. Average insert size: 1.3 kb (range: 0.5 - 3.0 kb). Referenced in Development 121, 2479-2489 (1995)"
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: whole embryo; Vector: pcMV-spORT; Site: SalI: Site:2 NotI; Cloned unidirectionally. Primer: Oligo dT. Gastrulating embryos were collected at 7.5dpc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="embryo"
/dev_stage="7.5dpc"
/lab_host="BH12S"
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/clone="IMAGE:541052"
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                                                                                                                                                                                                               Score 24.4; D
Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                                                                                 4; DB 9;
1.6e+06;
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mRNA sequence. BF582680

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TITLE
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                                                                                                                                                                                                                                                                  AUTHORS
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Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                              Hinxton, Cambridgeshire, CB10 ISA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus troplcalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas031111.sp6
                                                                                                                                                                                                                                                                                                                      Silurana tropicalis
Eukaryota, Metazoa, Chordata, Craniata, Ven
Amphibia, Batrachia, Anura, Mesobatrachia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs r@mail.nih.gov

Tissue Procurement: Jeffrey B.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                  1 (bases 1 to 49)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
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EST.
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NIH-WCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                     Sanger Centre
                                                                                                                                                                                                      Contact: Huckle E
                                                                                                                                                                                                                                                                                                        Xenopodinae; Silurana
                                                                                                                                                                                                                                                                                                                                                                                        western clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence
AL649742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Nus
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/clone_lib="MCI_CGAP_CO24"
/lab_host="DH10B (f1 phage-resistant)"
/focte="Organ: colon; Vector: powy-sports; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally, Prime: Oligo d
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is NCI_CGAP Library."
a 0 c
                 Location/Qualifiers
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Pred. No. 1.7e+06;
0; Mismatches 13;
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ia; Pipoidea; Pipidae;
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu040f06.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Huckle E
Sanger Centre
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Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
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                                                                                                                                                                  Similarity
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//note* Vector: pCS107; Site_1: EcoRI; Site_2: NotI: cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NoI at the 3' end."
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/clone="TGas031111"
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/dev_stage="neurula"
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/db_xref="taxon:8364"
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Pred. No. 1.7e+06;
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Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Teacheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids 1; Fabbles; Fabaceae; Papillonoideae; Trifolieae
                                                                                                                                        mRNA sequence.
AJ500588
AJ500588.1 GI:22081521
EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsei,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thesing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vj65h05.rl Knowles
clone IMAGE:933945
Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (Info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Technologies, Two different size selections: B1 (larger inserts) and B3. Two different size selections: B1 (larger 3 c 2 g 0 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="organ: embryo; Vector: pSPORT; Site_1: Noti; Site_2: Sali; Cloned unidirectionally from mNNA prepared from 800 blastocysts. primer: Sali(d7); 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTT-3'. cDNAs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cloned into the Noti/Sall sites of a pSPORT vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:933945"
/clone_11b="Knowles Solter mouse blastocyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J x DBA/2J F1"
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Solter mouse blastocyst BI Mus musculus CDNA
5', mRNA sequence.
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Rodentia;
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Pred. No. 1.7e+06;
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Krajinski,F., Manthey,K., Bartelsmeler,V., Meyer,F., Bartels,D.,
Bekel,T., Linke,B., Franken,P., Kuester,H., Perlick,A.M. and
                                                                                                                                                                                                                                            Dunn.D., Aoyagi.A., Barber.M., Beacorn.T., Duval.B., Hamil.C.
Islam.H., Longacre,S., Mahmoud.M., Weenen.E., Pedersen.T., Reilly
"M. Rose.M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright.D., Weiss,R. Stokes,R., Tingey,A., von Niederhausern,A.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                        University of Utah
University of Utah
                                                                                                                                                                                plasmid inserts
Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
1 (bases 1 to 50)
Dunn, D., Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
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Suppression Subtractive Hybridization (SSM). The SSM-CDNA 
fragments were generated using the SSM-adaptor sequences 
chaatcogscicactatagggcicagacgggcogaggt (Clontech) and 
chaatcogscicactatagggcycgggcycgaggt (Clontech) and 
ligated after Suppression Subtractive Hybridization in to 
the pCEM-Tassy vector from Promega. Plasmids containing 
CDNA inserts were propagated in E. coli TOP 10F' cells
                                                                                                                       Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'tissue_type='mycorrhizal rootis'
/dev_stage='3 weeks after inoculation',
/dev_stage='3 weeks after inoculation',
/dev_stage='3 weeks after inoculation',
from roots harvested three weeks after inoculation with
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/db_xref-"taxon:3880"
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                                                                                                                       Polymers Research Bldg.,
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                   Std Error: 0.00
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University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
                                                                                                                                                                                                                                                                                                                          Takeuchi, I., Kohara, Y. and Tanaka, Y.
Population analysis of cDNAs from unicellular and multicellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: 0467 row: L. column: 09
Seq primer: CACACAGGAAACAGCTATG
Class: plasmid ends
High quality sequence stop: 50.
                                                                                                                                         Tel: 81-298-53-4664
Fax: 81-298-53-6614
                                                                                                                                                                                                                                                                                Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
AU268686
AU268686.1 GI:20527484
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                                                                                                                                                                                                                                                          Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                   stages of Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                       Urushihara, H., Morio, T., Saito, T.,
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mycetozoa; Dictyostelilda; Dictyostelium (bases 1 to 44)
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                                                                                                                hideko@biol.tsukuba.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis, vector DNA was prepared from a derivative of pNRA2 (git4722114(gib.RE129072.1), a copy-number induvible derivative of plasmid Rl. The vector was ligated with edaptors complementary to the insert adaptors and purified. The sherred, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adaptored vector DNA, and transformed into chemically-competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."

1 c 1 g 47 t
                         /strain-"AX4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
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/clone="UUGC1M0467L09"
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/strain="C57BL/6J"
                                            /organism="Dictyostelium
                                                                                            Location/Qualifiers
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RESULT 12
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AL587734/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roslin, Midlotlin, HBJS 9PS, UK
Tel: +44 (0)131 527 420
Tex: +44 (0)131 527 420
Fax: +44 (0)131 420 0434
Email: frazer:murray@bbstc.ac.uk
GCGGCCCTTTTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria: Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae: Gallus:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dept. Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Frazer Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP Chicken Brain Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murray, F.
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AL587734
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/clone=lib="VS"
/clone=lib="VS"
/sex="mat A"
/sex="mat A"
/dev_stage="vegetative"
/dev_stage="1 g 1;
                                                                                                                                                                                                                                                       /note-"Vector: pSPORTI; Site_1: Noti; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGCCCCCTTFTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech (*6654-1)" 33 t 1 others
                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Brain"
/dev_stage="Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="ROS061D09"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="BP Chicken Brain Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gallus gallus"
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70.5%;
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                                                                                                                                                                                         Score 23.8; DB 9;
Pred. No. 2.1e+06;
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                         Email: cgapbs-r@mail.nih.gov
                                         Contact: Robert Strausberg, Ph.D.
                                                          Unpublished (1999)
                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
                                                                                                        Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                             mRNA sequence.
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                                                                                                                                                                                                                                                                               BF692288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://lmage.llnl.gov
Plate: LLCM1198 row: b column: 15
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BF691166
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National Institutes of Health, Mammalian
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Lissus_type-"melanotic melanoma, high MDR"
/lab.hoss-"bludB (TI phago-resistant)"
/note-"Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:4332206"
/clone_11b="NIH_MGC_62"
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Pred. No. 2.1e+06;
0; Mismatches 12;
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-6639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU107269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., He, Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
l (bases l to 50)
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LNG09312, mRNA sequence
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., Nakamura, Y., Suyama, A. and Sugano, S.
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(Where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.94 0 kb). 15/15 colonies
contained inserts by PGR, This library was enriched for
full-length clones and was constructed by Cloncach
Laboratories (Palo Alto, CA)."
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Double-Stranded CDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'.CACGGCCATTWNTGCCC-3' and 3' adaptor
sequence: 5'.CATTCTMGAGGCGCAGGGGGCCGACATG-GT(30)BN-3'
                       /organism="Homo sapiens"
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/clone="LNG09312"
/clone_lib="Sugano Homo sapiens cDNA library"
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| 642 GGTGGCTGAAAAAAAGGGAAGGTGCTCAGGAAGGCTAAGAGCAT 4
                                                                                                        842 GGTGGCTGAAAAACGGGAAGGAGTTTAAGCAGGAGCATCGCAT 884
                                                                    Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki.y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and Characterization of a full length-enriched and
a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
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50 bp mRNA linear EST 30-AUG-200
AU107270 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
LNC09789, mRNA sequence.
AU107270
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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dimethylfumarate treated U937 cells"
18 c 7 g 17 t
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GenCore version 5.1,3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

December 11, 2002, 16:33:52 ; Search time 7159 Seconds (without alignments) 1756.297 Million cell updates/sec US-09-954-556-3 Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Searched:

Scoring table:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 50

GenEmbl:\* Database

em\_ov:\* em\_pat:\* em\_ph:\* em\_pl:\* em\_ro:\* em\_sts:\* em\_or:\* 

em\_v1:\*
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em\_htgo\_mus:\* em\_htgo\_other:\*

TITLE JOURNAL FEATURES

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

PAT 04-DEC-1998 Unclassified.
Unclassified.
Seno,M.W. Watchabe,T. and Igarashi,K.
Watch-soluble mutein of FGF receptor, DNA and production thereof
Patent: US 5750371-A 15 12-MAY-1998;
Location/Qualifiers linear DNA AR007163 39 bp 1 Sequence 15 from patent US 5750371. AR007163 GI:3966647 Unknown. Unknown. RESULT 1 AR007163/c LOCUS DEFINITION ACCESSION SOURCE ORGANISM REFERENCE AUTHORS VERSION

source

BASE COUNT ORIGIN

Matches

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TK25-fibroblast growth factor receptor [3' region] [human, normal lenkooyee DNA, Genomic, 36 nt, segment 1 of 2].
                                  PRI 09-MAY-2000
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              36 bp DNA linear PRI 09-MAY-26 BEK-fibroblast growth factor receptor [3' region] [human, normal sq.135, 54.35]
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GenBank staff at the National Library of Medicine created this GenBank staff gibbsq 41355] from the original journal article. This sequence comes from Fig. 4b.
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0.6%; Score 27.4; DB 9;
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                                                                                   Score 33; DB 6; Length 39;
Pred. No. 4.6e+03;
3; Mismatches 3; Indels
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Patent: US 5589451-A 15 31-DEC-1996;
Location/Qualifiers
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187104.1 GI:3206822
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l Similarity 84.6%;
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1 (bases 1 to 30)
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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TITLE Methods of assaying differential expression JOURNAL Patent: US 5994076-A 431 30-NOV-1999; EARUDES LOCALION/Qualifiers Lass COUNT 3 a 10 c 7 9 5 t ORIGIN	Owery Match  0.6%; Score 25; DB 6; Length 25;  Bact Local 25; Lonservative 0; Mismatches 0; Indels 0;  Qy 768 GCTCCANGCTGGCGGGCCAAC 792  Db 1 GCTCCANGCTGGCGCGAAC 25		Unknown. Unclassif I (bases Chenchik, Methods o Patent: U	BASE COUNT 3 a 7 c 11 g 4 t	RESULT 10	đ)	Ouery Match 0.6%; Score 25; DB 6; Length 25; Best Local Similarity 100.0%; Pred. No. 3.88+65; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 768 GTCCATGCTGCCAGGGGCAAC 792
Ouery March Best Local Similarity 96.64; Pred. No. 1.1e.05; Bast Local Similarity 96.64; Pred. No. 1.1e.05; Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 2546 GANTUTCHOSTCTORACARGARGAA 2577 Db 1 GAATTCTCACCAACCAATGAGGTA 29		ORGANISM synthetic construct source location/Qualifiers 1. 30   Organism="synthetic construct"   Adb_xref="taxon:12630"   6 t   ORIGIN 5 a 8 c 11 9 6 t	Owery Match 0.6%; Score 25.8; DB 6; Length 30; Best Local Similarity 93.18; Pred. No. 2.5e+05; Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0; QY 248B TGTTGGCATGCCTCCAGAAAC 2516  Db 30 TGCTGGATGCATGCCTCACAGAGC 2516  Db 30 TGCTGGATGCATGCCTCACAGAGAC 2	RESULT 7 A29211.C LOCUS LOCUS LOCUS LOCUS LOCUS ACCESSION Oligonucleotide OAE984 from patent W09111459. ACCESSION A29211.1 G1:1248932 KEYWORDS SYNTHEALC CONSTRUCT. ORGANISM AIGHT SHIPLE CONSTRUCT. FRAVINES  FRAVILES ACCESSION A29211.1 G1:1248932 ACCESSION A2	NT 5 a Match Match Scal Similari S 27; Cons	TGTTGGCATGCACTGCCCACACACC 2516	VERSION AR090311.1 GI:10017066 SCHORS SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 25) AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.

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PAT 05-DEC-1998
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Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchina;
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    Hominidae; Homo
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[1] (bases 1 to 31)
[Cargilli, W. Iroland, J.S. and Lander, E.S. Human single nuclectide polymorphisms
Patcher; WO 0166800 A 956 13-58P-2001
[Patcher; WO 0166800 A 956 13-58P-2001]
[Cargilli, MHITBIRGO, INSTITUTE POR BOMBLICAL RESEARCH (US)
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3. 6.7e+05;
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/db_xref="taxon:6306"
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Pred. No. 6.2e+05;
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Sequence 4 from patent US 5783683.
AR019665 GI GI:3974779
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Sequence 84 from Patent WO0196584.
AX347734
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/db_xref="taxon:9606"
a 13 c 12 g
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Morrison, R.S.
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Eukaryota: Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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ALBERT EINSTEN COLLEGE OF WEDICINE OF YESHIVA UNIVERSITY (US)
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/db_xref="taxon:32630"
/note="potential mutagenic oligonucleotide"
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Chenchik, A., Jokhadze, G. and Bibliashvilli, R.
Wethods of basaying differential expression
Patent: US 6352829-A 432 05-MAR-2002;
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                                                    Sequence 432 from patent US 6352829.
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Sequence 958 from Patent WO0166800.
AX248879
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Sequence 9 from Patent WO0107627.
AX077808
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Query Match 0.6%; Score 23.6; DB 6; Length 42; Best Local Shilarity 76.3%; Pred. No. 9.2e-02; Marches 23; Conservative 0; Mismatches 9; Indels

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Wilson,S.E. Treaments for corneal healing with hepatocyte and keratinocyte growth factors
Patent: US 5889451-A 15 31-DEC-1996;
Location/Qualifiers
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Wilson, S. Methods and treatments for corneal healing with growth factors
Patent: US 5703947-A 18 30-DEC-1997;
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SH Unclassified (25)
Unclassified (25)
CE 1 (bases 1 to 25)
DRS Chenchk, A., Jokhadze, G. and Bibliashvilli.R.
B. Methods of assaying differential expression
RBAL US 599407-6, 423 20-NOV-1999;
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